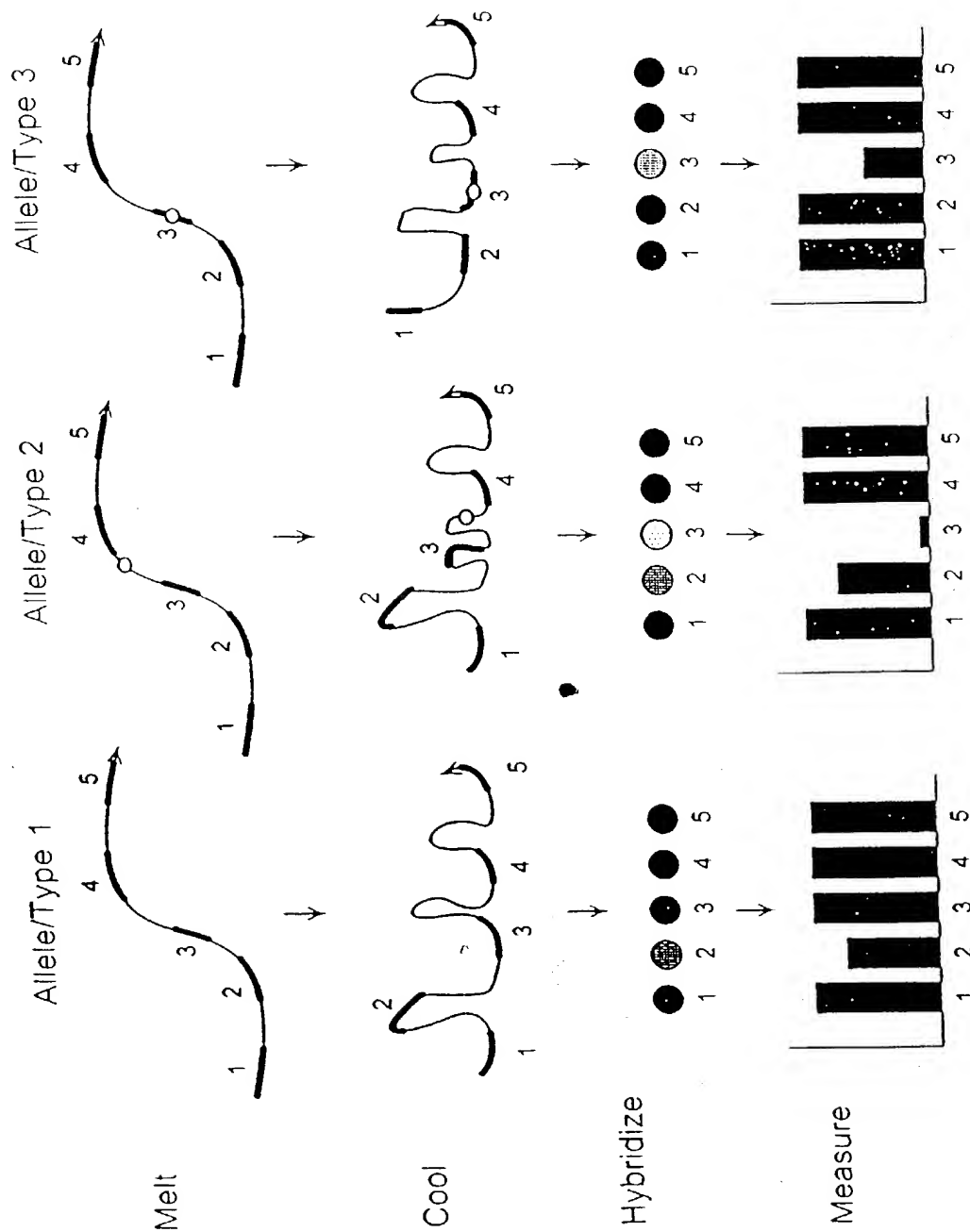


FIGURE 1



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FIGURE 2

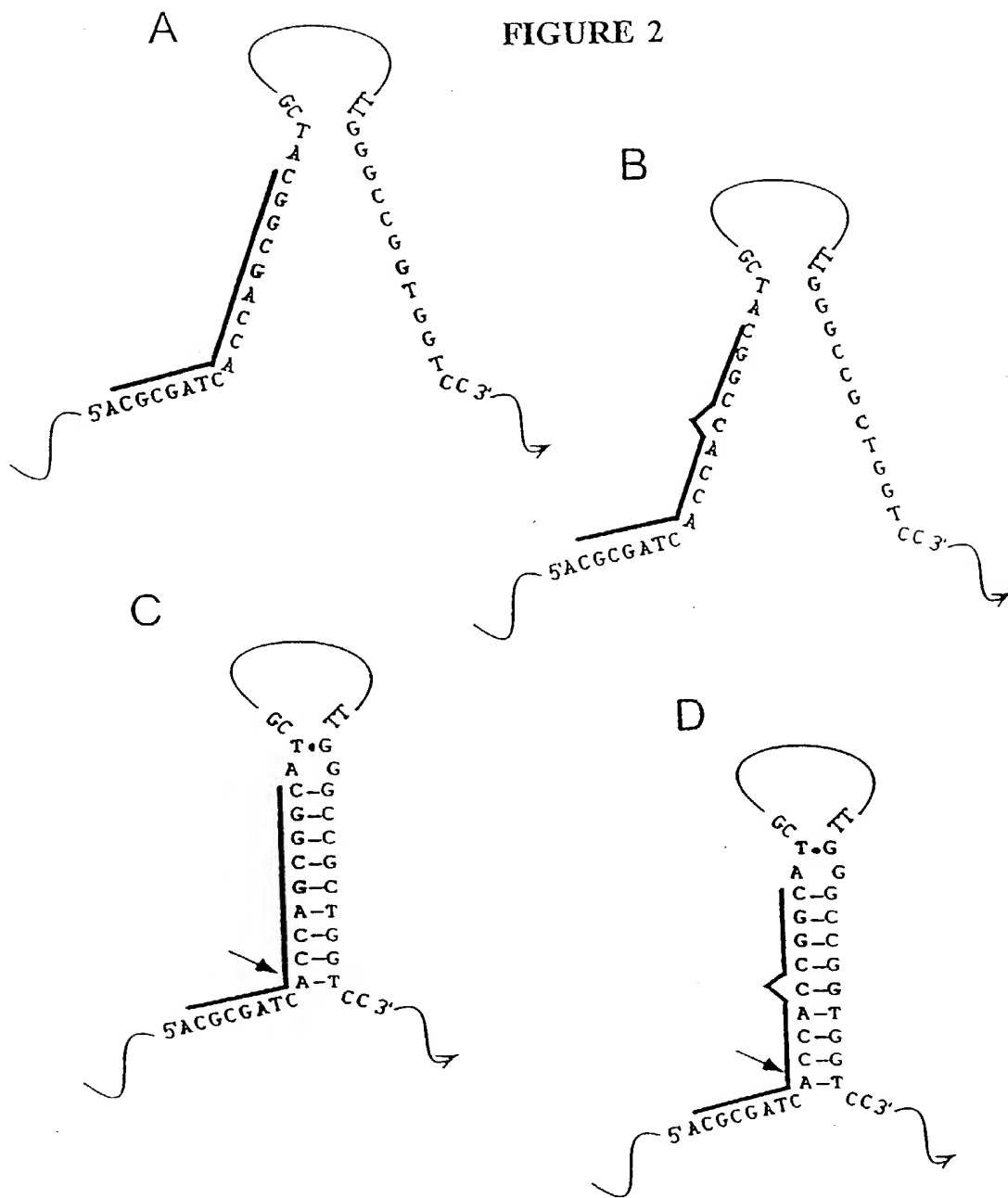


FIGURE 3

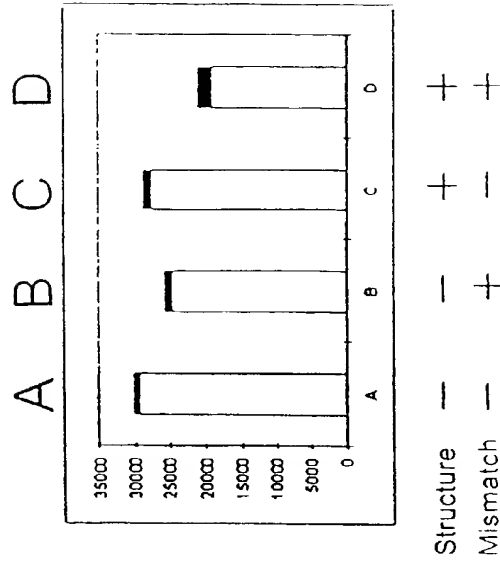
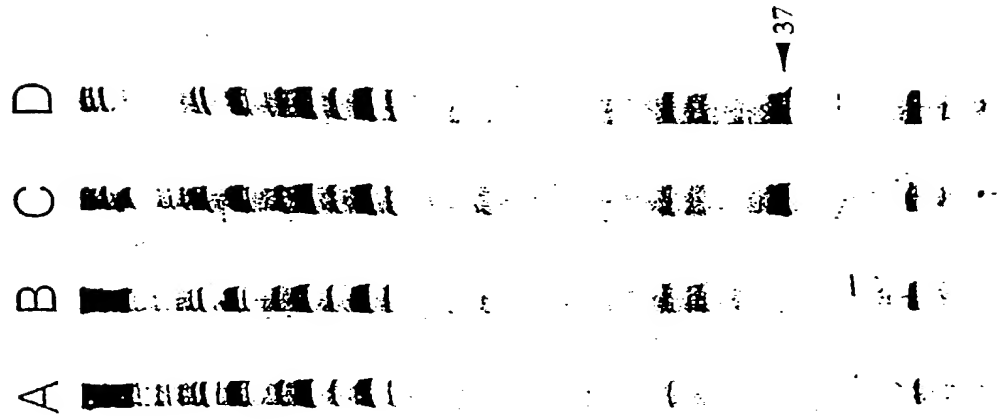
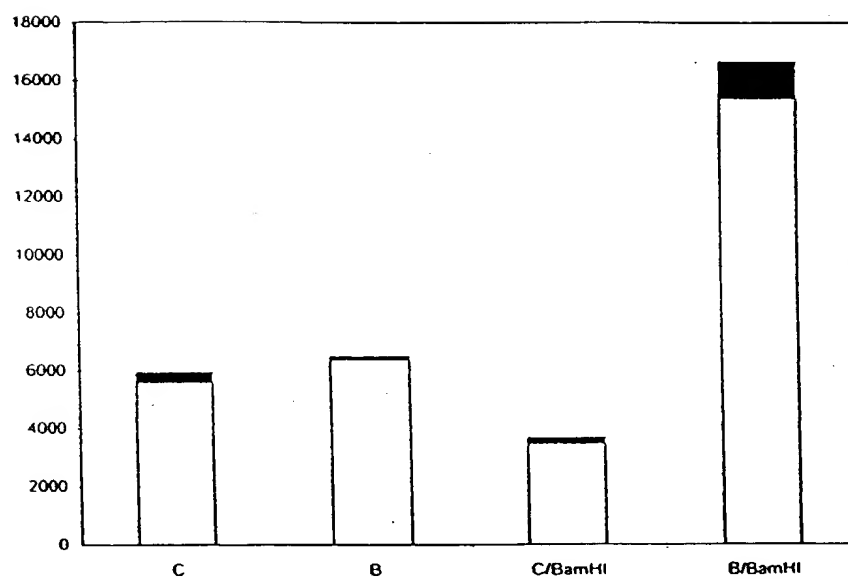


FIGURE 4



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FIGURE 5



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FIGURE 6

Consensus:	GATTCTGTCT	TCACGCAGAA	AGCGTCTAGC	CATGGCGTTA	GTATGAGTGT	CGTGCAGCCT
HCV 1a	-----	-----	-----	-----	-----	-----
HCV 1b	-----	-----	-----	-----	-----	-----
HCV 2c	-----	-----	-----	-----	-----	-A-----
HCV 3a	-----	-----	-C-----	-----	-C-----	-----

	#249	#251
CCAGGACCCC	CCCTCCCGGG	AGAGCCATAG
-----	-----	TGGTCTGCGG
-----	-----	AACCGGTGAG
-----	-----	TACACCGGAA
-----	-----	-----
-T-----	-----	-----
-----	-----	-----
-C-----	-----	-----
-----	-A-----	-----

#253	#257
TTGCCAGGAC	GACCGGGTCC
-----	TTTCTTGGAT
-----	CAACCGGCTC
-----	AATGCCCTGA
-----	GATTGGGCG
-----	-----
-----	-----
-G--A--	-T-----
-C--TG--GT	-A--A--
-----	-G-----
-----	-A--CA--

#40	#261	#263
TGCCCCCGCA	AGACTGCTAG	CCGAGTAGTG
-----	-----	TTGGGTGCGG
-----	-----	AAAGGCCTTG
-----	-----	TGGTACTGCC
-----	-----	-----
-G-----	-----	-----
-----	-----	-T-----
-G-----	-TCA--	-----
-----	-----	-----
TGATAGGGTG	CTTGGGAGTG	CCCCGGGAGG
-----	-----	TCTCGTAGAC
-----	-----	CGTGCAATC
-----	-----	-----
-----	-A-----	-----
-----	-----	-----

FIGURE 7

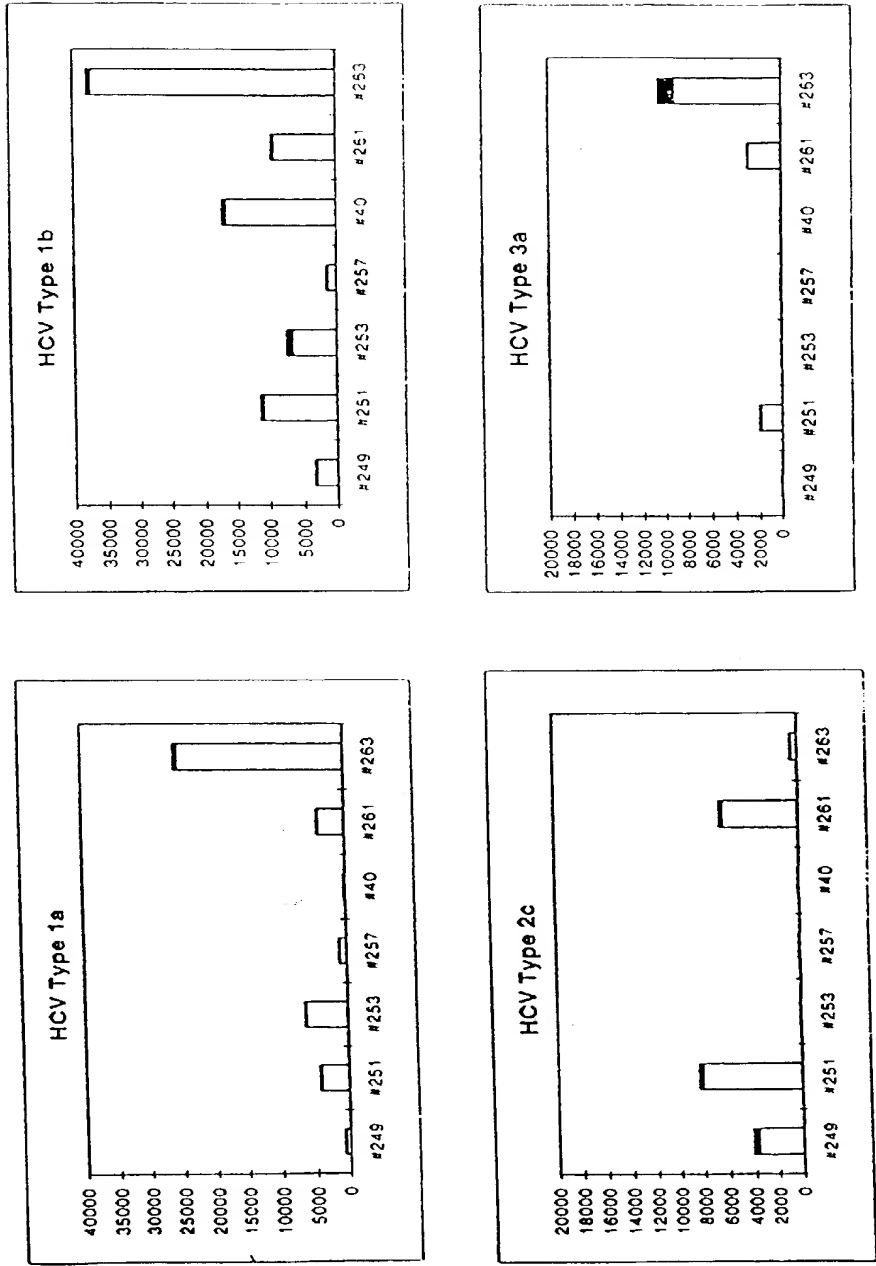
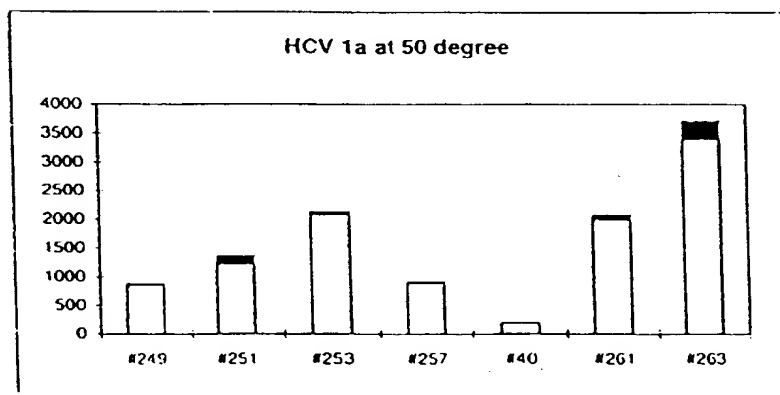
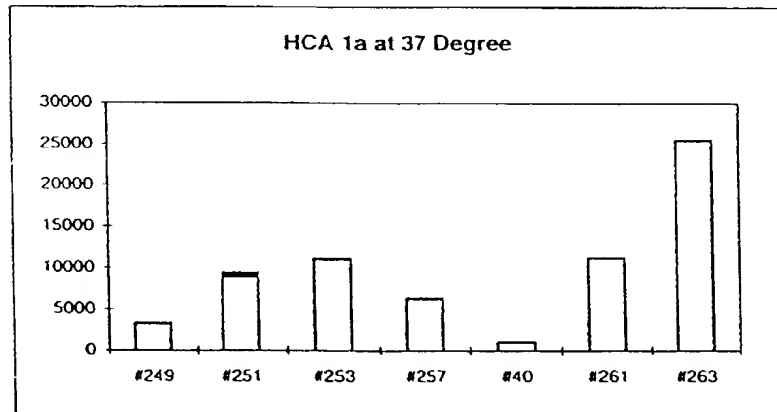
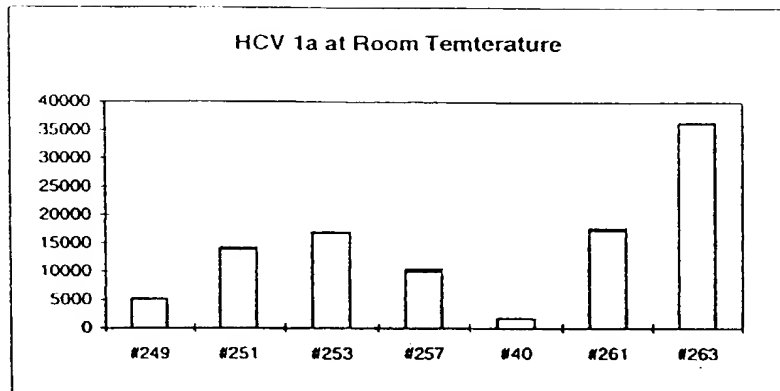
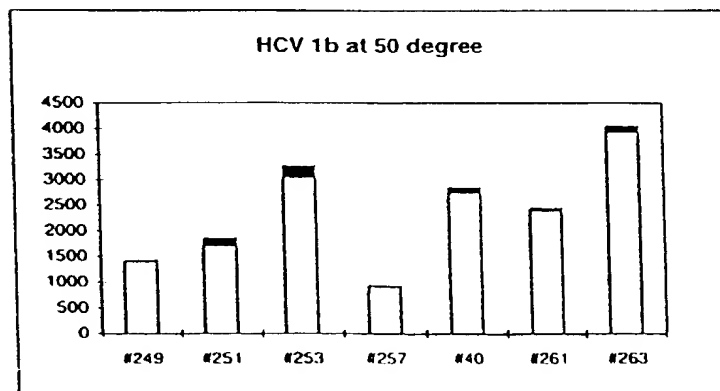
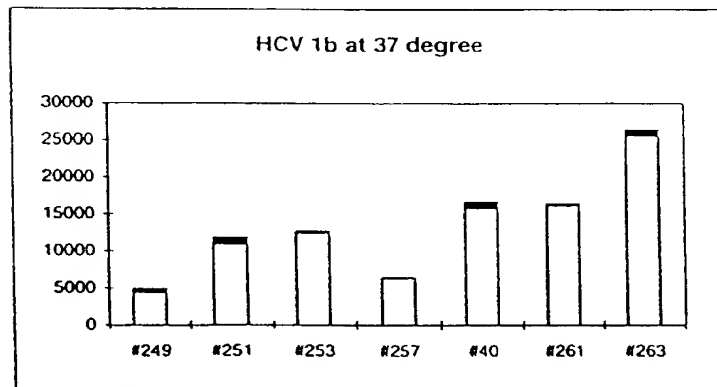
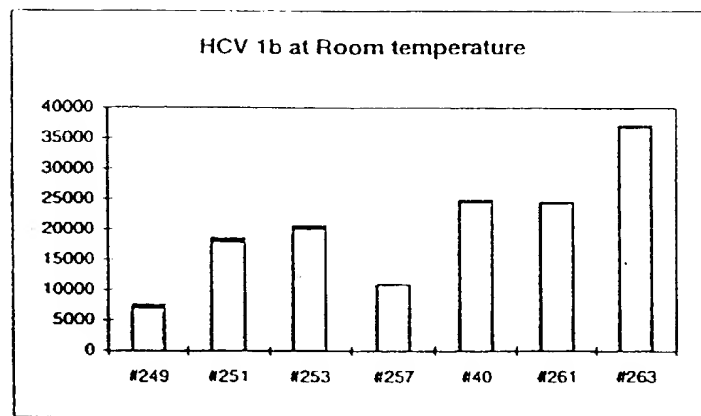


FIGURE 8A



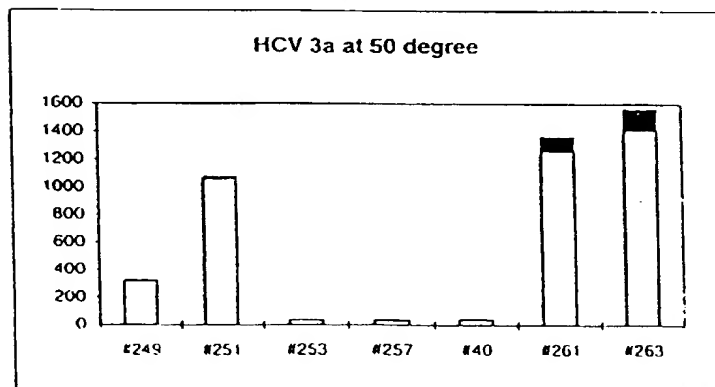
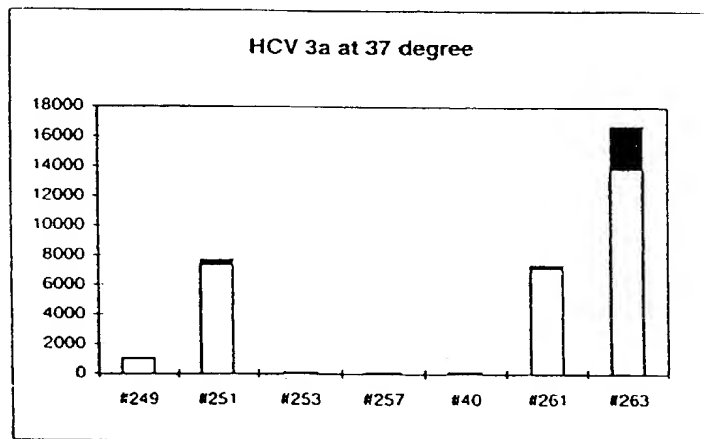
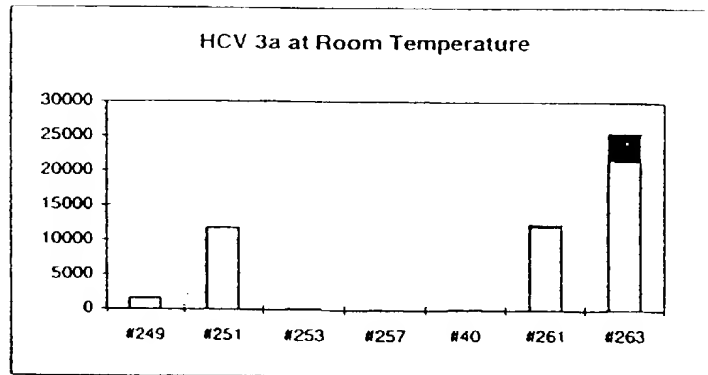
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FIGURE 8B



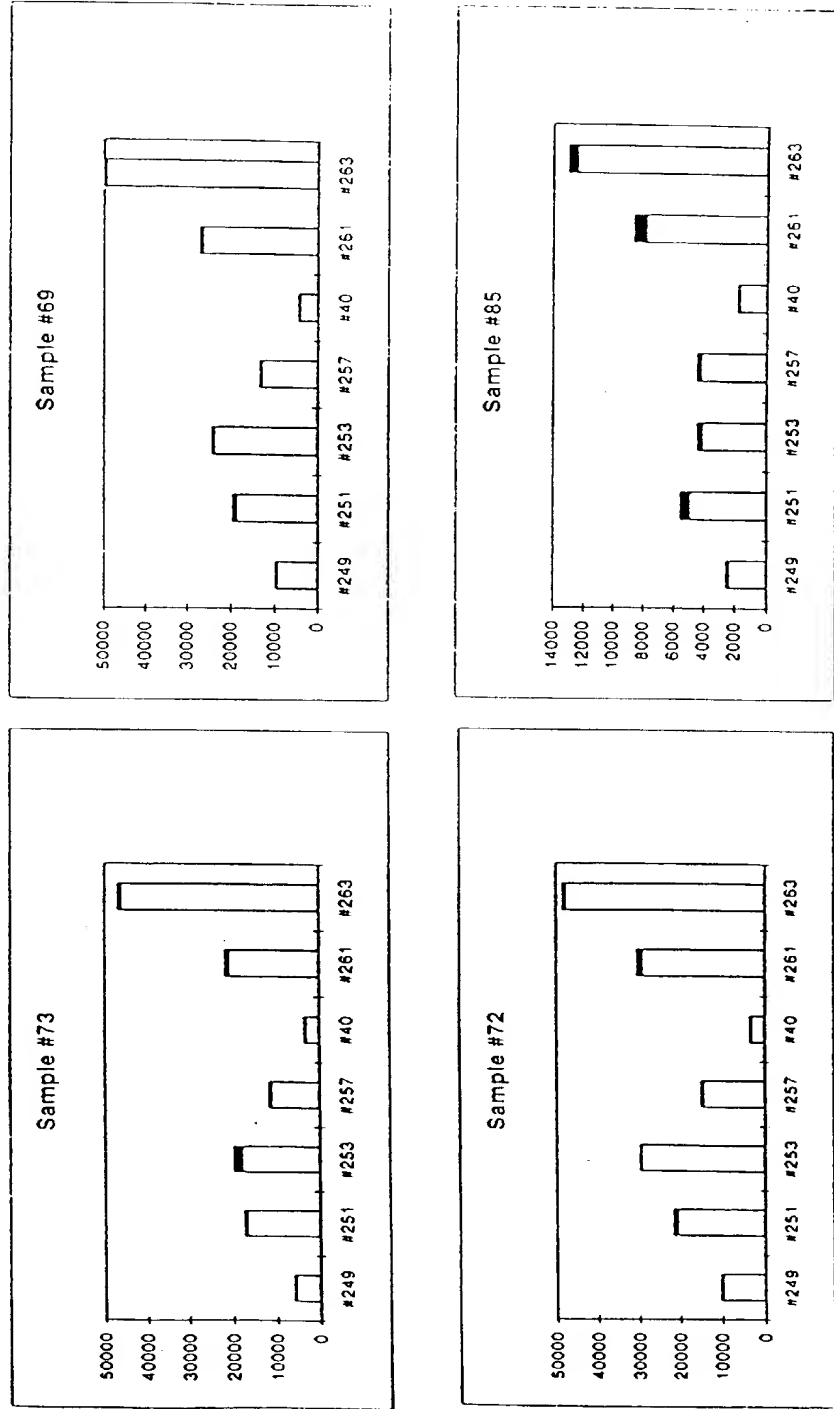
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FIGURE 8C



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FIGURE 9A



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FIGURE 9B

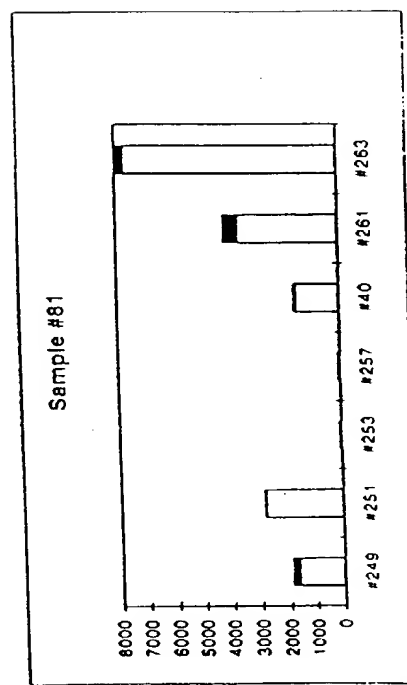
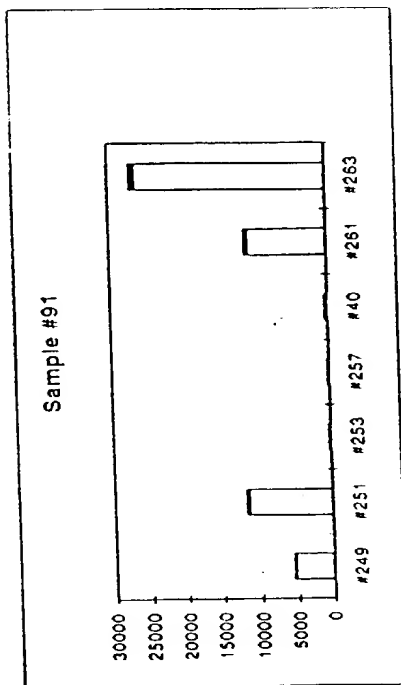
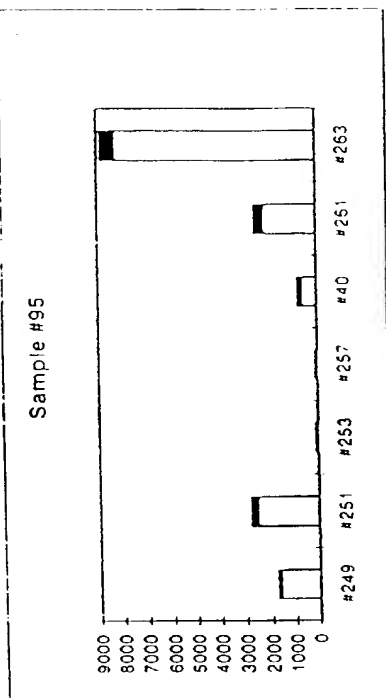


FIGURE 9C

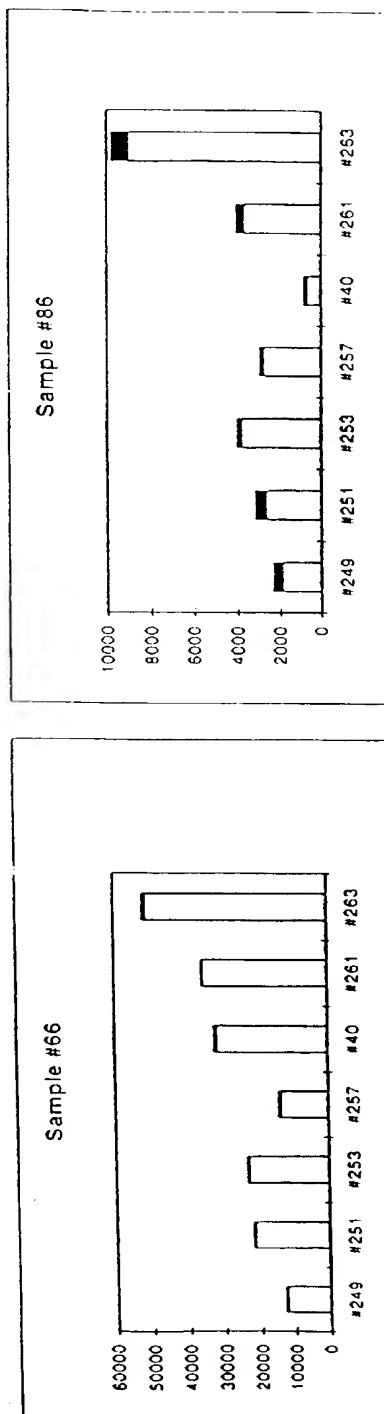
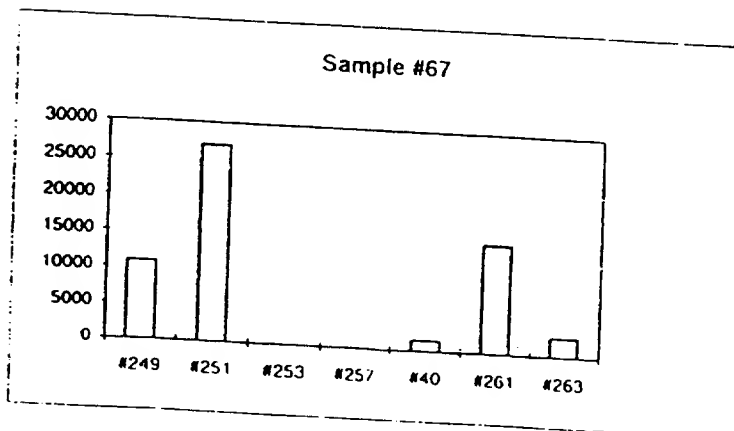
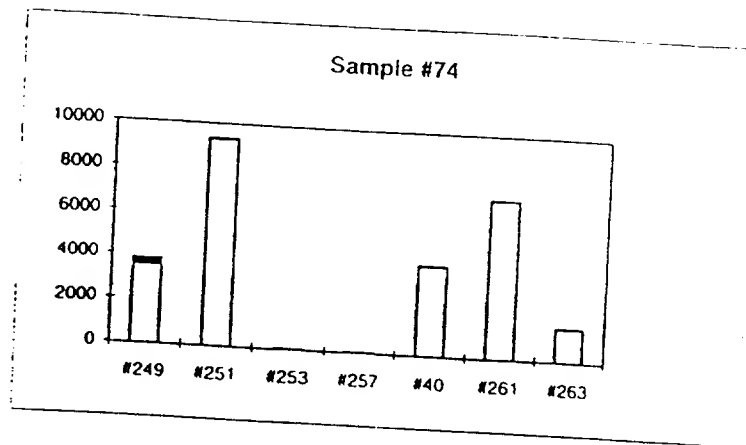


FIGURE 9D



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FIGURE 10

#80

A
G A
T - A
C - G
T - A
G - C
T - A
C - G
G - C
C - G

5'-FTGCTCTCTGGT TGGTCTCTCGTAAT-3'

#81

A
G A
T - A
C - G
T - A
G - C
T T
C C
G - C
C - G

5'-FTGCTCTCTGGT TGGTCTCTCGTAAT-3'

#82

G^{AA}
T T
C T
T T
G T
T T
C T
G C
C

5'-FTGCTCTCTGGT TGGTCTCTCGTAAT-3'

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09883045 061501
TOST90" sh628860

FIGURE 11A

#2) 5' Biotin

	I	
	T	A
C	G	A
A	T	A
G	C	G
A	T	A
C	G	C
A	T	A
G	C	G
C	G	C
G	C	G

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#FD91) 3' Biotin - CGAGAGACCA - 5'

	A	
G	A	
T	A	
C	G	
T	A	
G	C	
T	A	
C	G	
G	C	
C	G	

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - AGACCATTACCAGA -Biotin 5'

#4) 3' - GAGACCATTACCAGAG -Biotin 5'

#79) 3' - AGAGACCATTACCAGAGA -Biotin 5'

↓ ↓

#116) 3' - AGAGACCAACCAGAGA -Biotin 5'

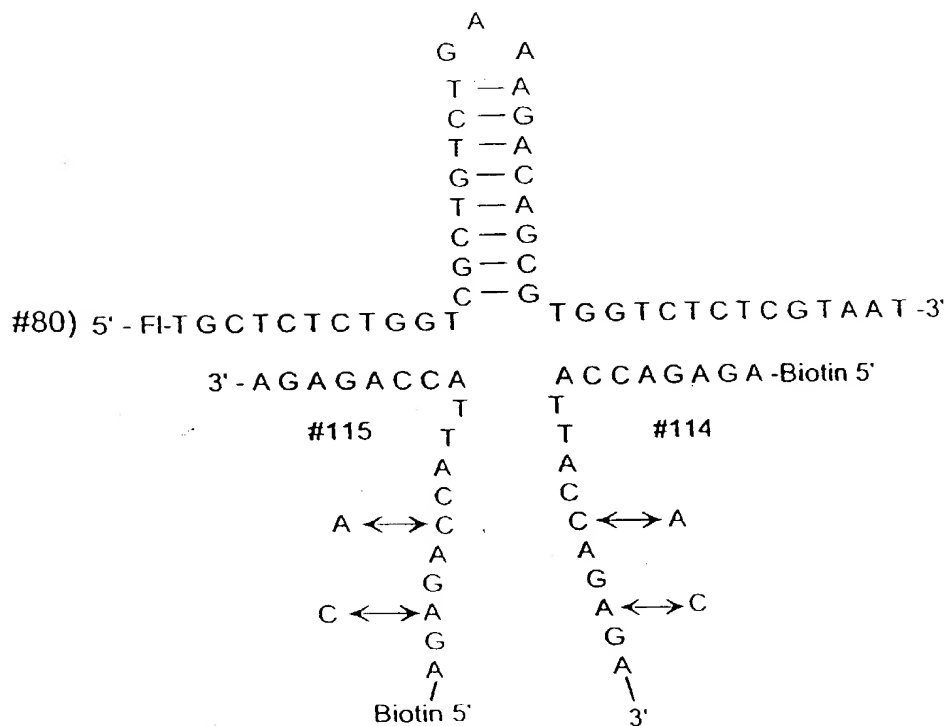
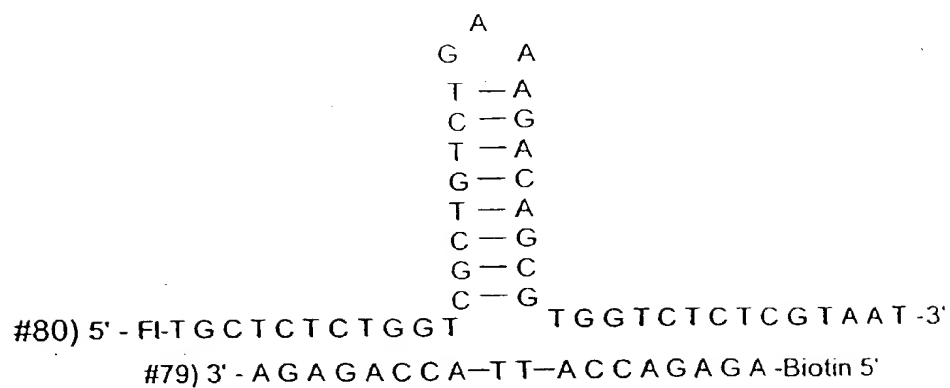
#117) 3' - TACCAGAGA -Biotin 5'

#118) 3' - AGAGACCAT - 5'

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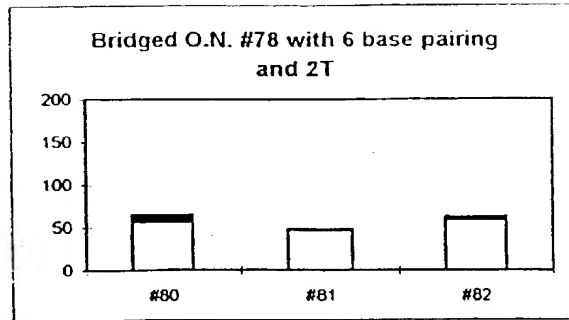
FIGURE 11B



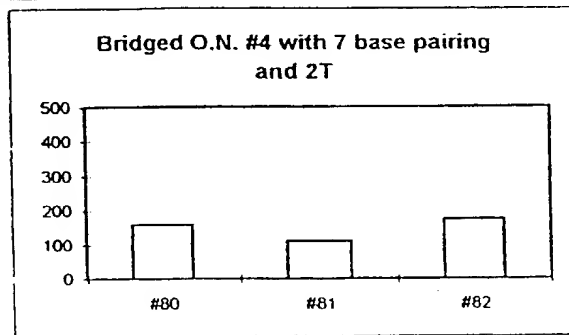
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FIGURE 12

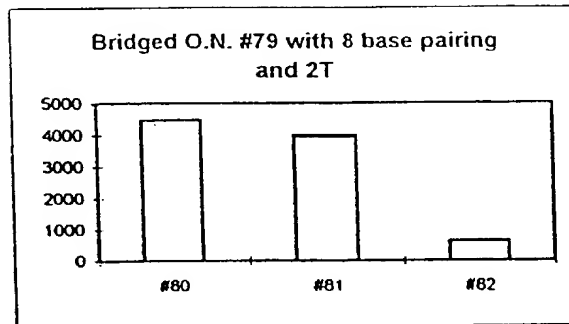
A



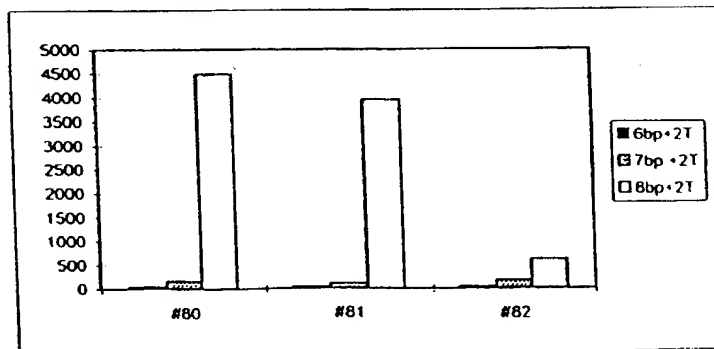
B



C

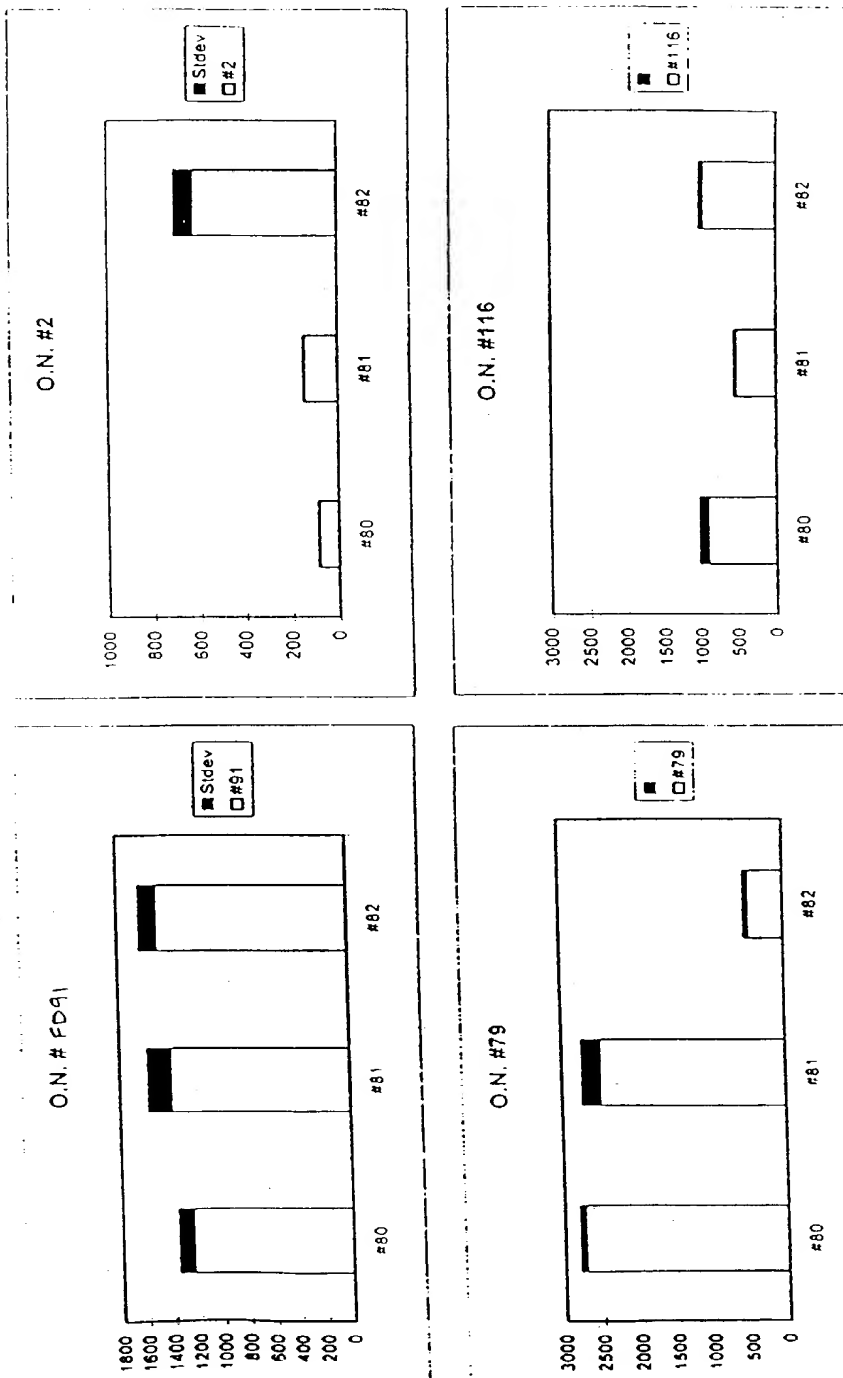


D



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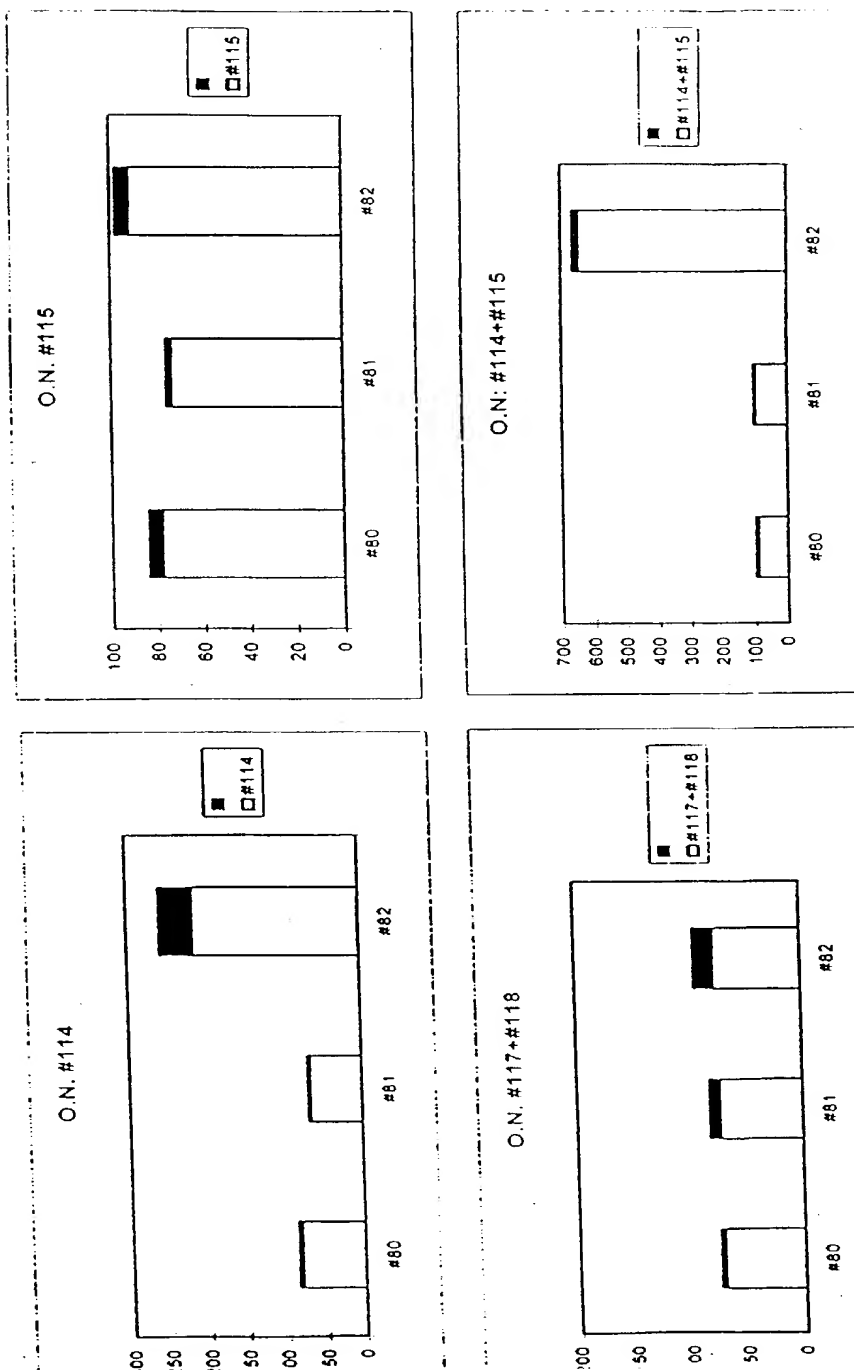
FIGURE 13A



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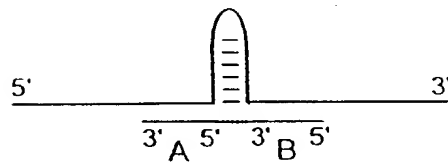
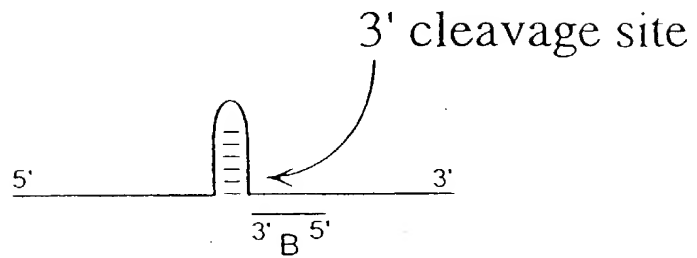
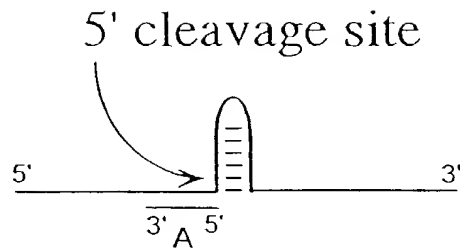
FIGURE 13B

POST 90" SHEET 3353



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FIGURE 14



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```

1-----10-----20-----30-----40-----50-----60-----70-----80
1a CTCGAAAGCACCCTATCAGGCAGTACCACAAAGGCCCTTTCGGGACCCACACTACTCGGCTAGCAGTCTTGGGGGGCAGG
1b .....
2a/c .....A.....G.....
3a .....TGA.....C.....

-----90-----100-----110-----120-----130-----140-----150-----160
1a CCCAAATCTCAGGCATTGAGCGGTTTATCCAAAGAAAGGACCGGTCGCTCGGCAATTCCGGGTGTACTCACC GGTTCC
1b .....G.....
2a/c .....GG.....A.....T.....C.....
3a .....T.....GT.....AC.....CA.....G.....

-----170-----180-----190-----200-----210-----220-----230-----240-----
1a GAGACCACTATGCTCTCCCGGAGGGGGGCTCCTGGAGGCTGCACGACACTCATATAAGCCCATGGCTAGACGCTTTCTGCG
1b .....
2a/c .....G.....T.....
3a .....G.....

```

FIGURE 16A

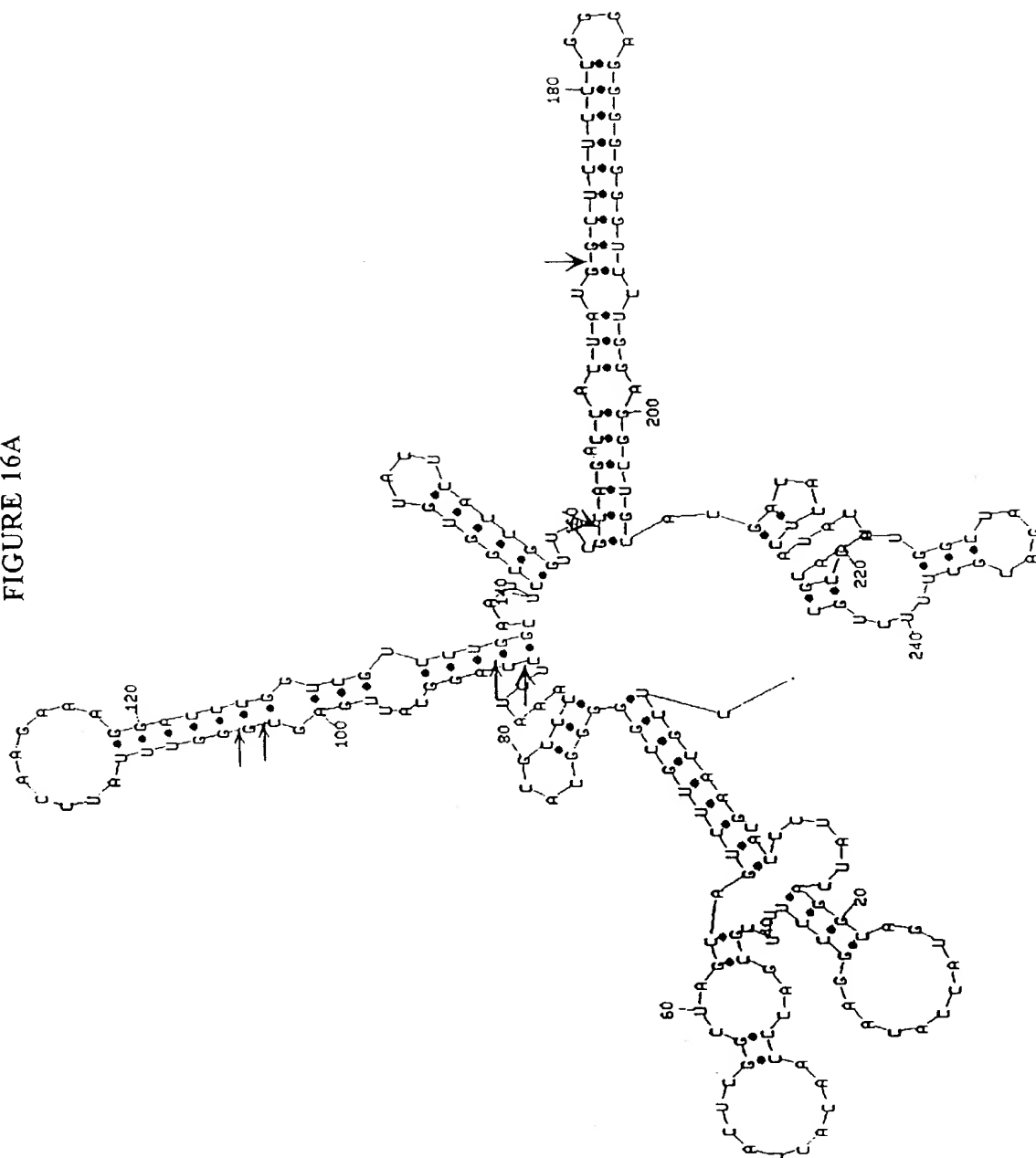
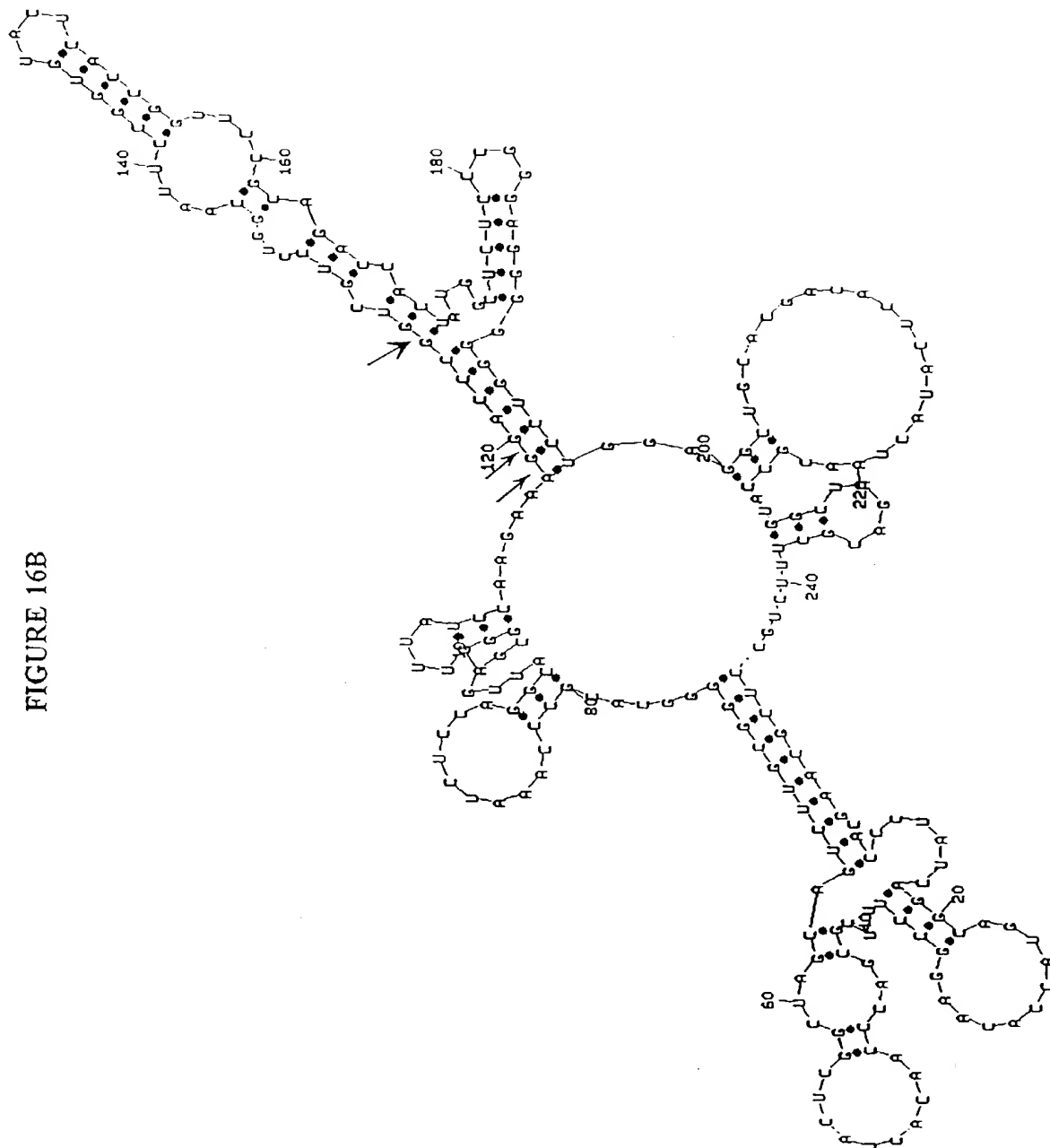
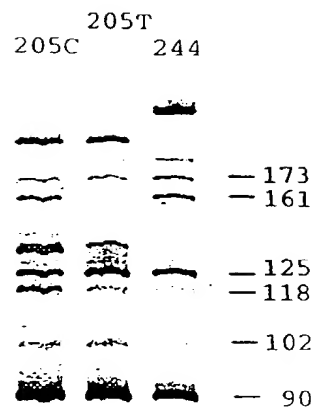


FIGURE 16B



09882945.001504
T05T90" 54628860

FIGURE 17A



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FIGURE 17C

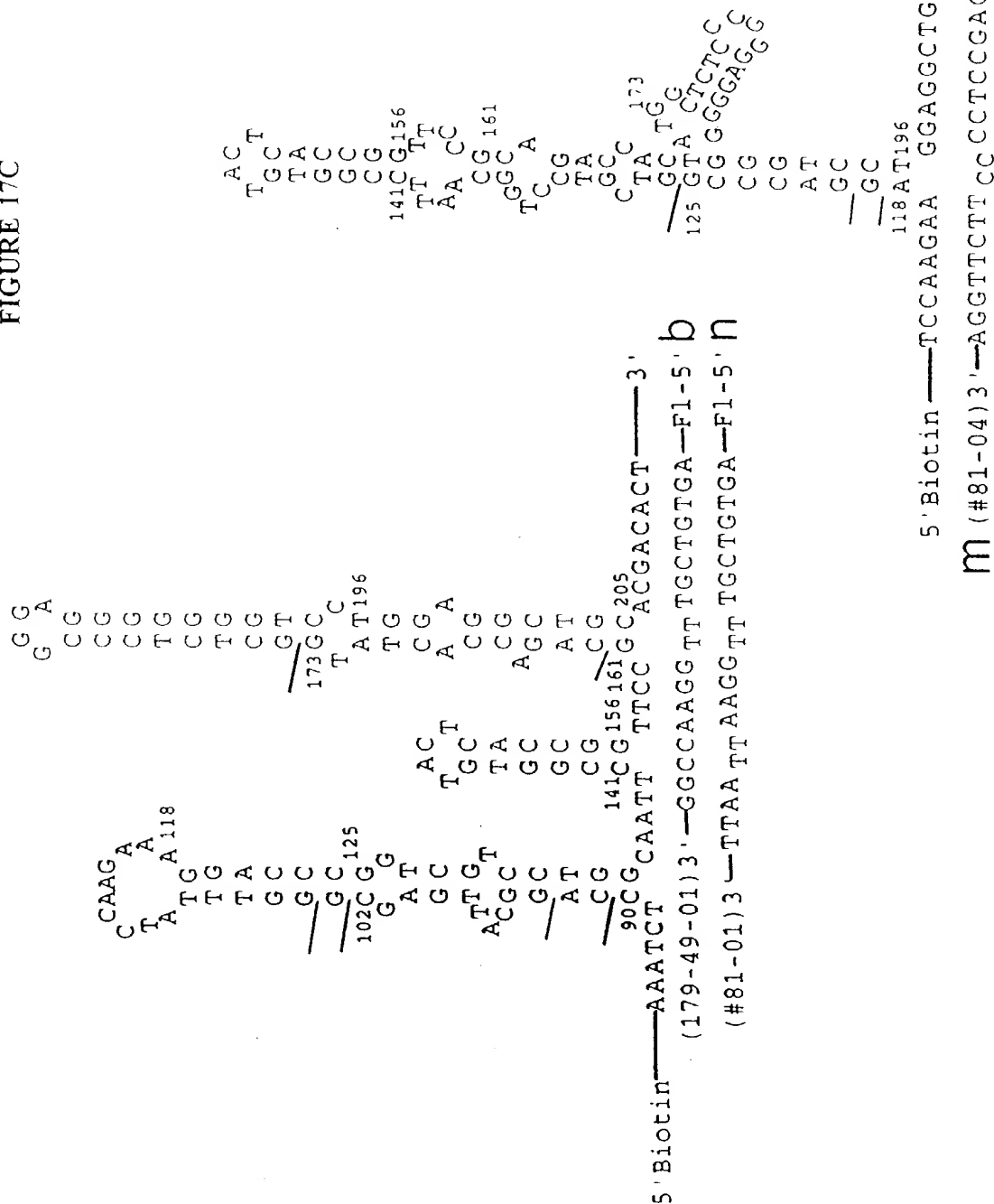
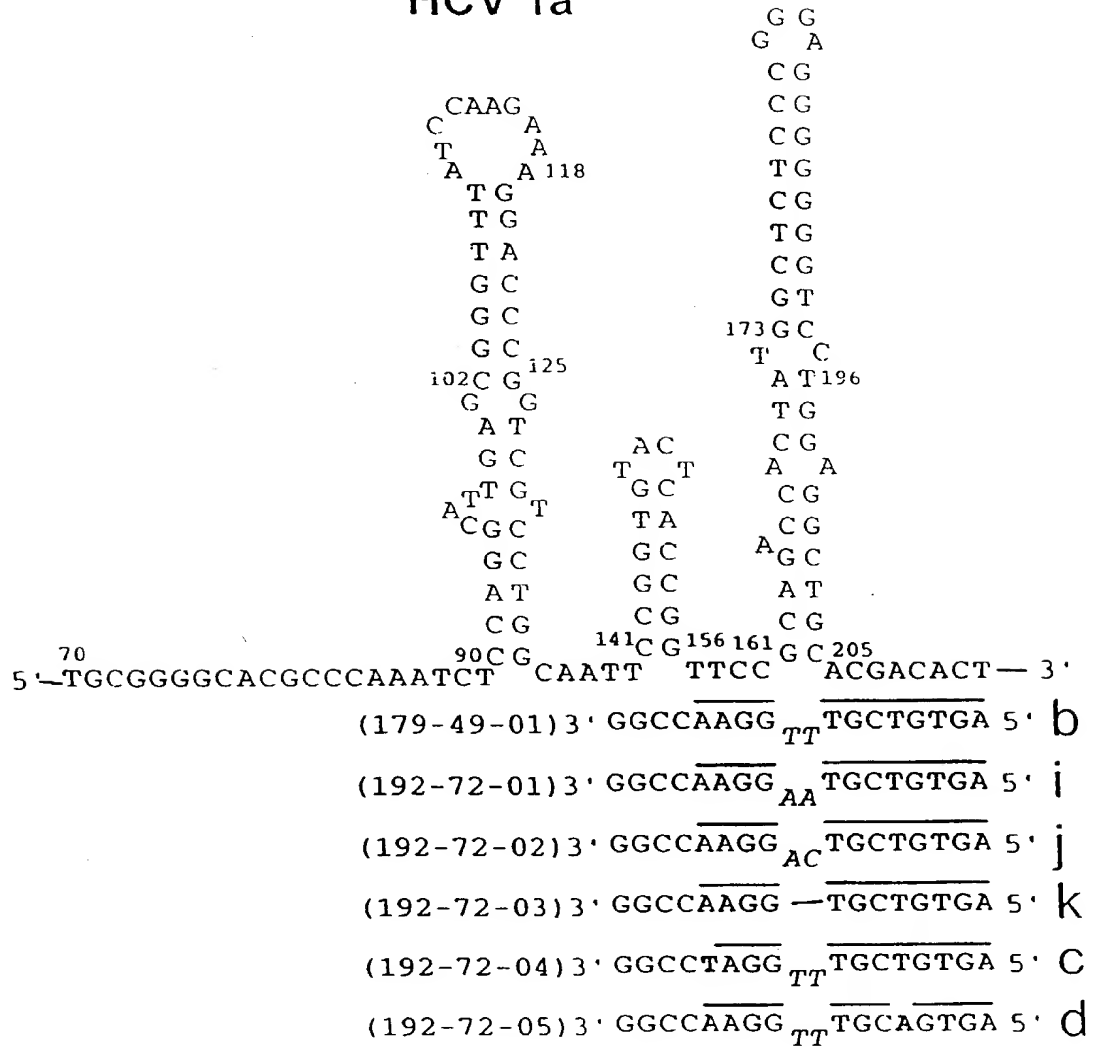


FIGURE 18A

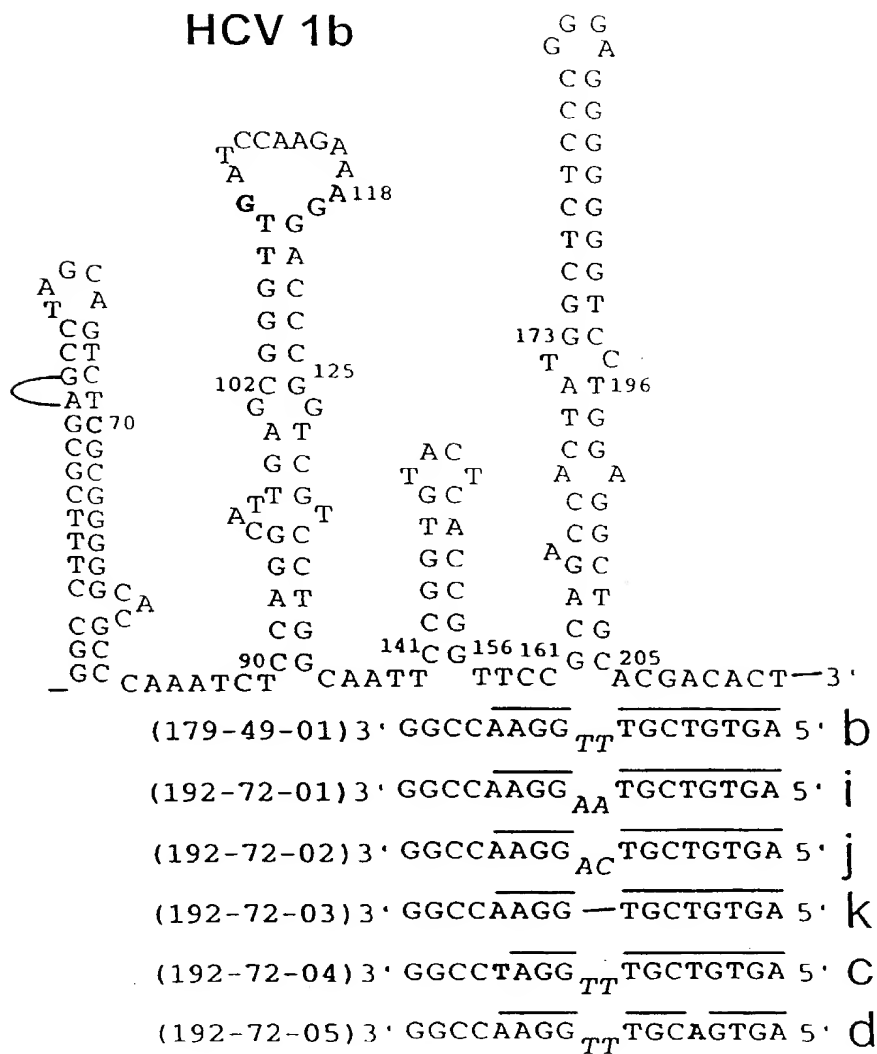
HCV 1a



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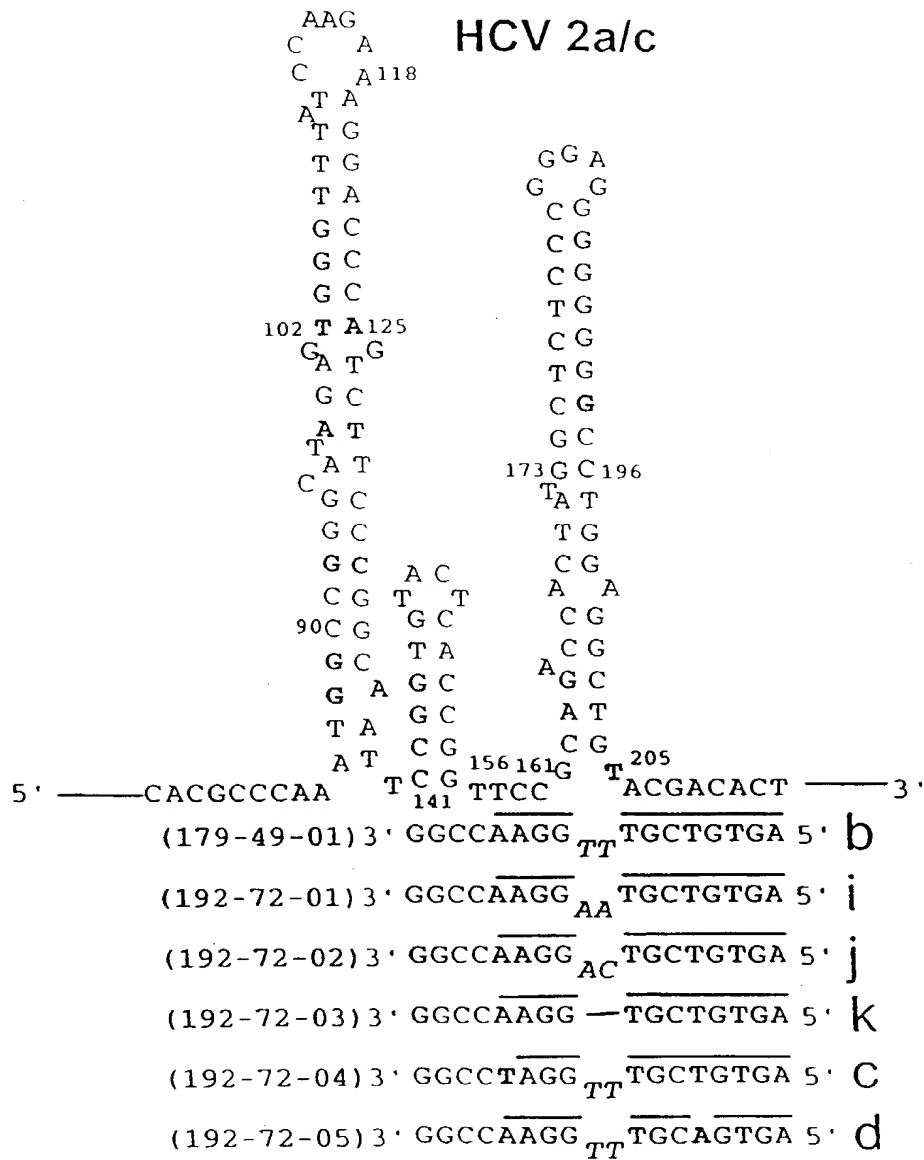
FIGURE 18B

HCV 1b



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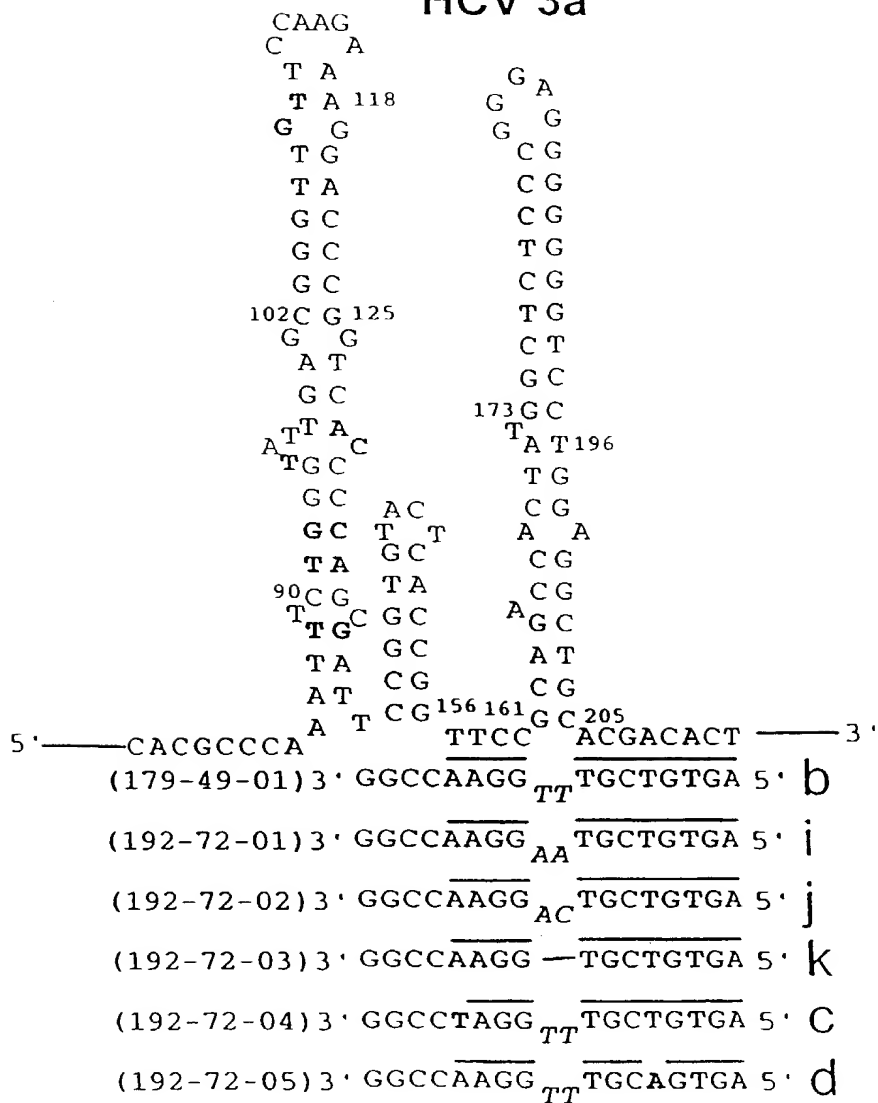
FIGURE 18C



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FIGURE 18D

HCV 3a



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FIGURE 19

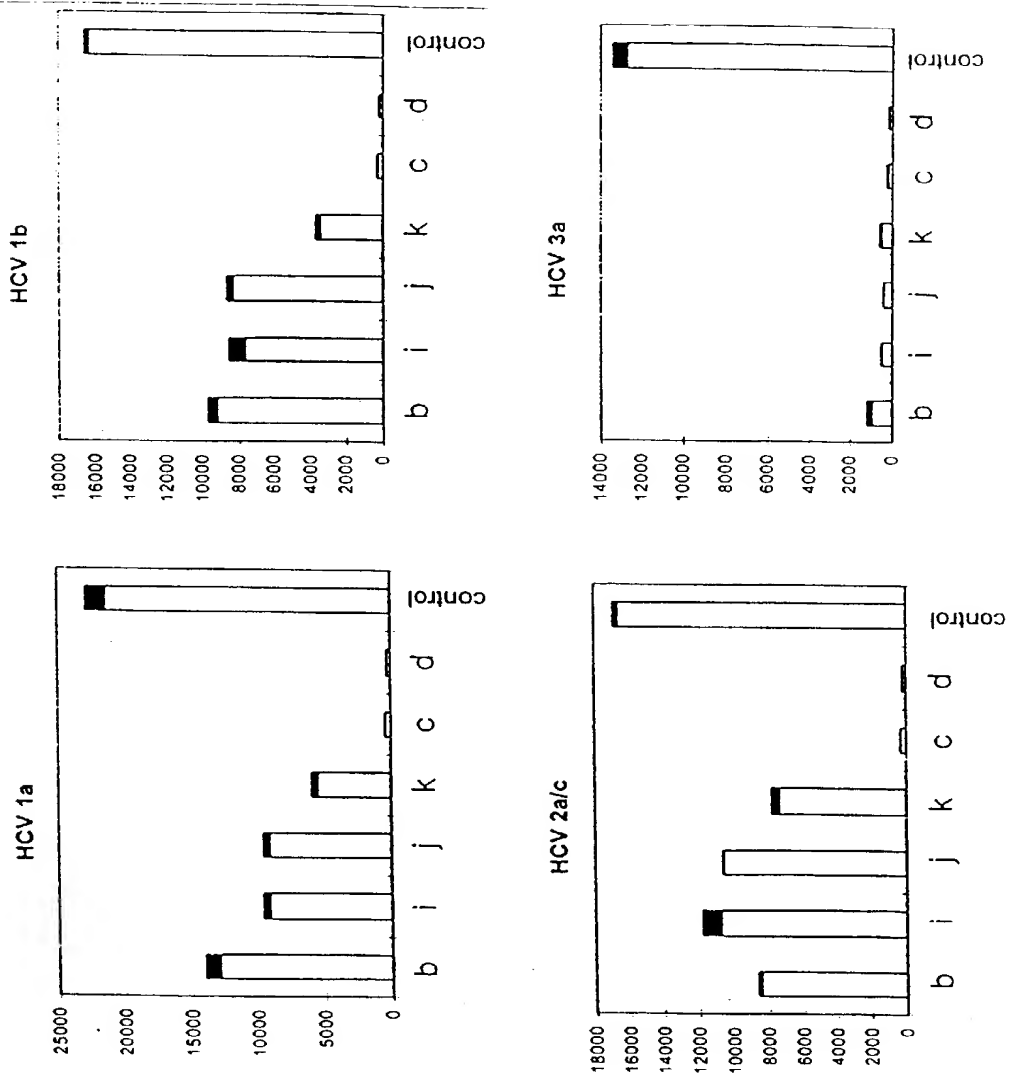


FIGURE 20A

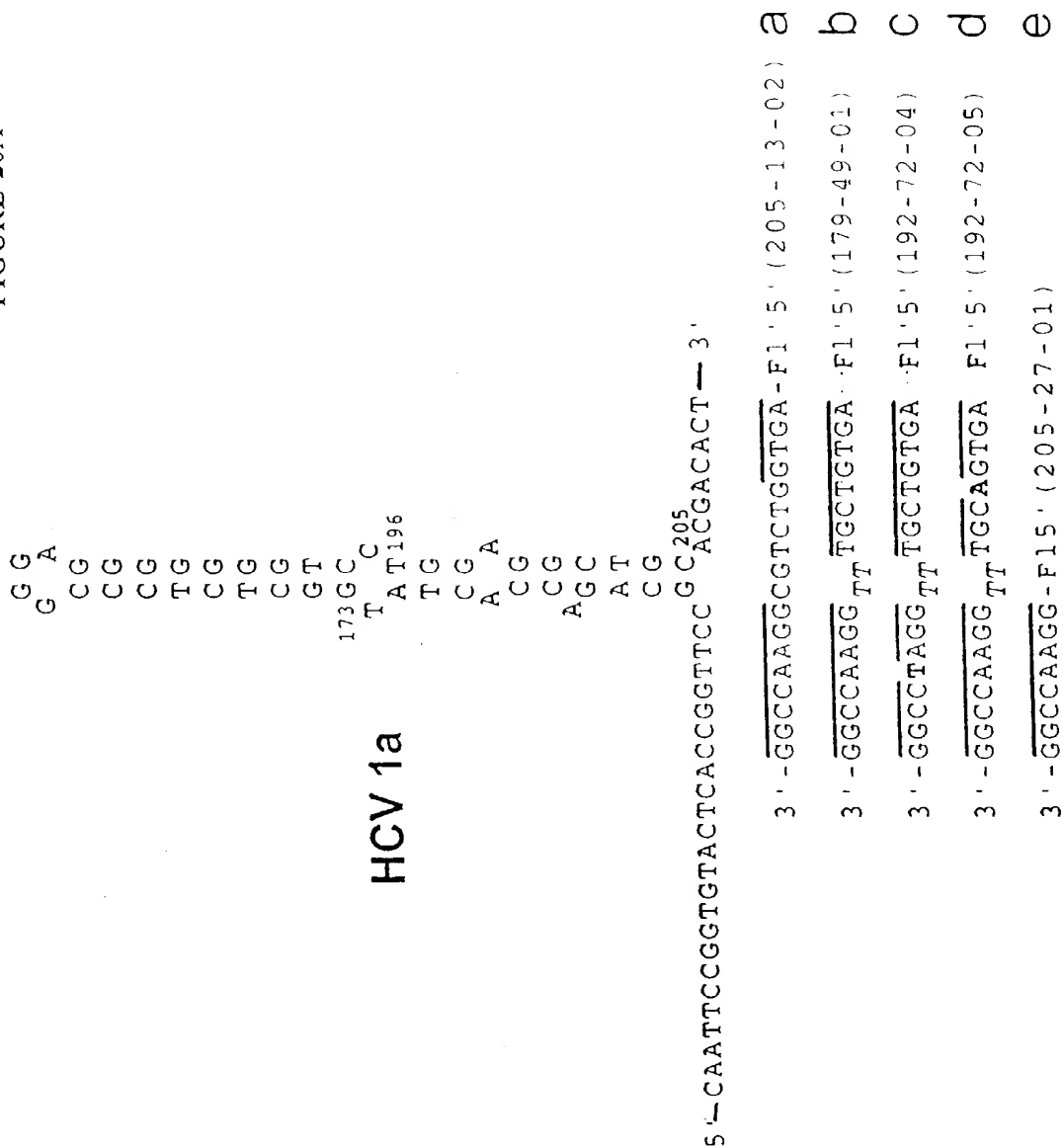
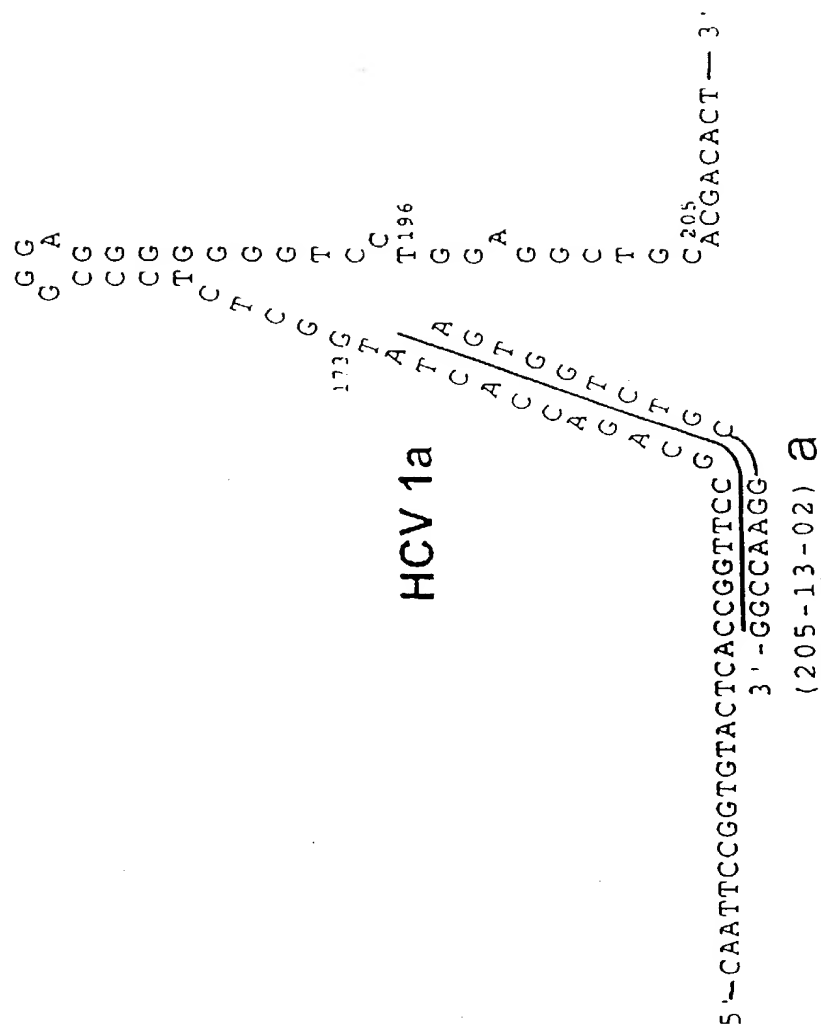


FIGURE 20B



Parameter	Value	Unit
Temperature	25.0	°C
Pressure	1.0	atm
Flow rate	1.0	L/min
Wavelength	254	nm
Scan rate	1.0	nm/min
Integration time	1.0	s
Resolution	0.5	nm
Detector	Photodiode array	
Injection volume	10	μL
Injection port	1	
Column	Agilent Zorbax SB-C18	
Column length	150	mm
Column diameter	4.6	mm
Column packing	5 μm	
Mobile phase	Water/Acetonitrile	
Mobile phase ratio	90/10	
Flow rate	1.0	mL/min
Retention time	12.5	min
Peak area	1.2	10 ⁶
Peak height	0.8	10 ⁴
Peak width	0.5	min
Peak symmetry	1.0	
Peak resolution	1.5	
Peak purity	99.9	%
Peak identification	100	%
Peak confidence	100	%
Peak quality	100	%
Peak signal	1.0	10 ⁴
Peak noise	0.1	10 ⁴
Peak baseline	0.0	10 ⁴
Peak drift	0.0	10 ⁴
Peak shift	0.0	10 ⁴
Peak jitter	0.0	10 ⁴
Peak skew	0.0	10 ⁴
Peak tailing	0.0	10 ⁴
Peak fronting	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	10 ⁴
Peak kurtosis	0.0	10 ⁴
Peak excess kurtosis	0.0	10 ⁴
Peak skewness	0.0	10 ⁴
Peak excess skewness	0.0	1

FIGURE 21

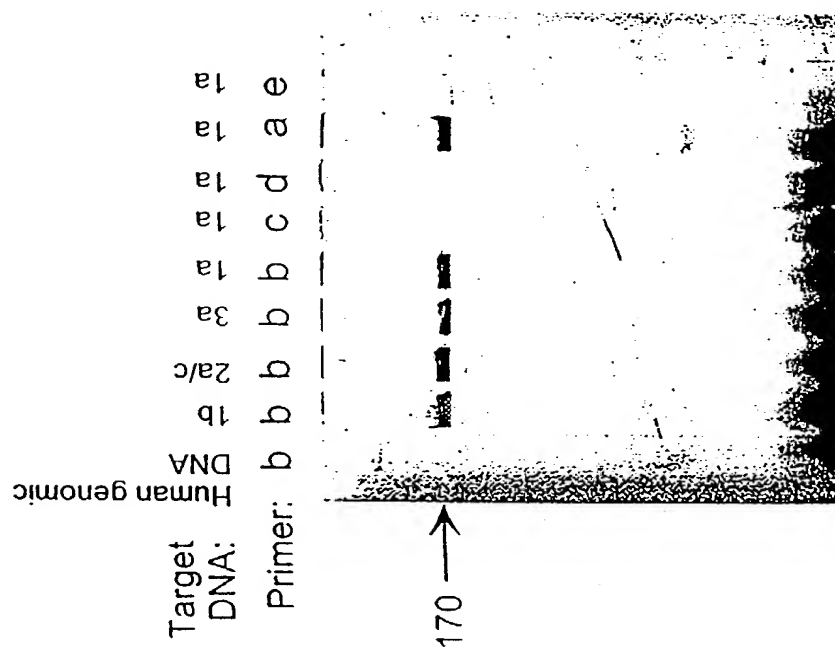


FIGURE 22

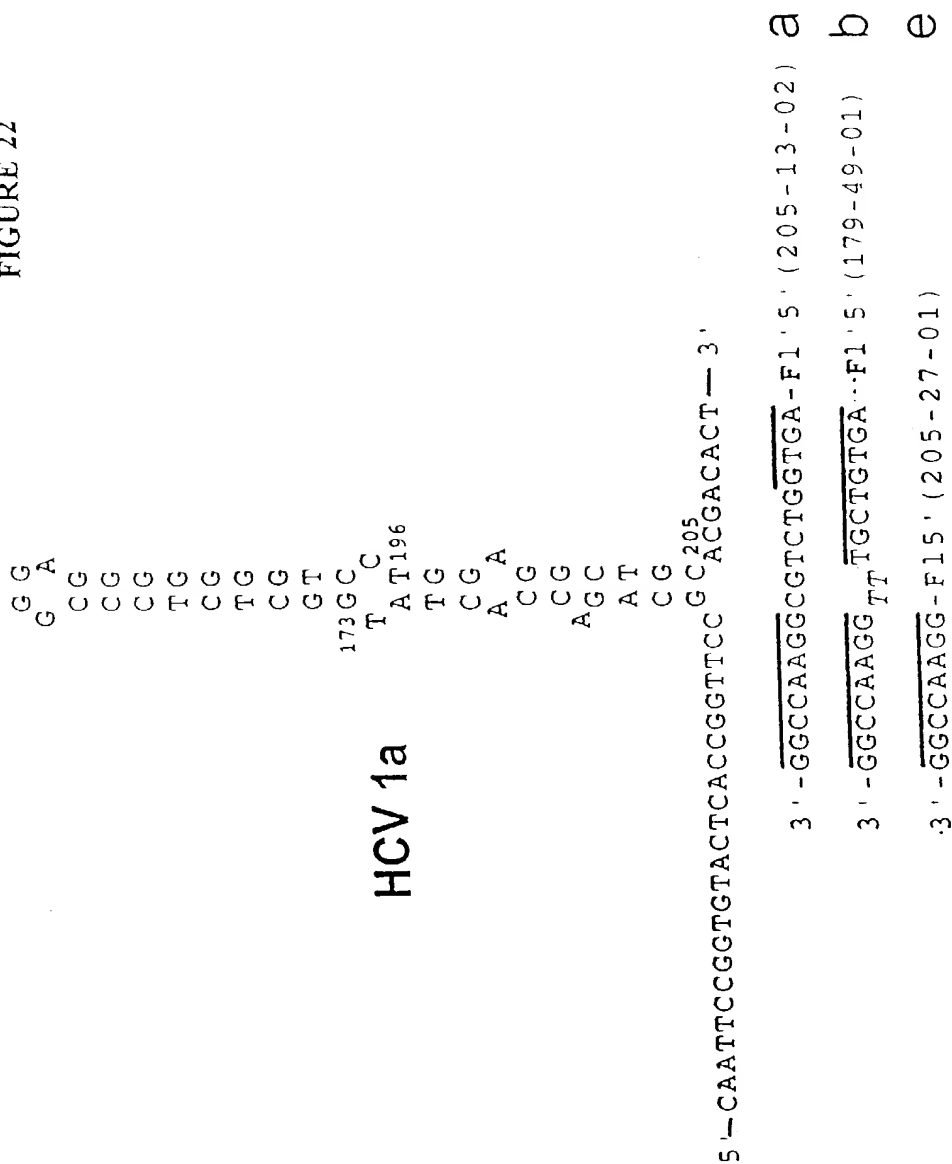
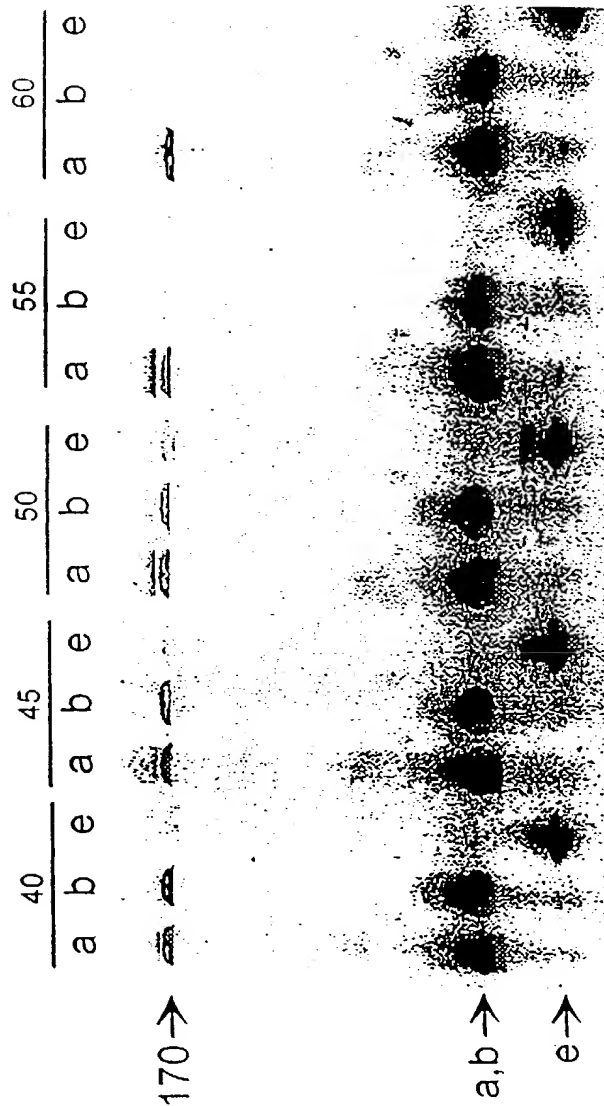
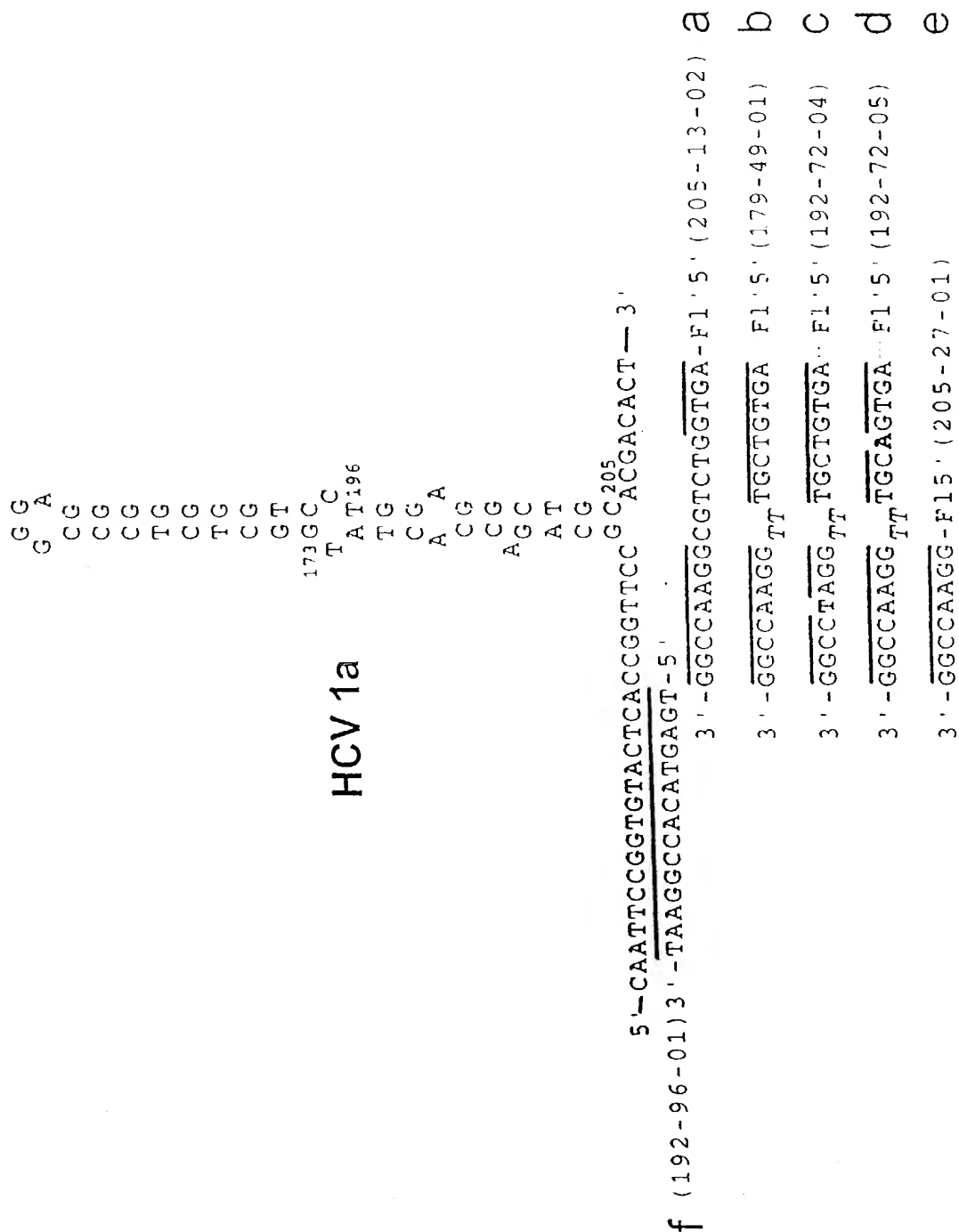


FIGURE 23



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FIGURE 24



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FIGURE 25

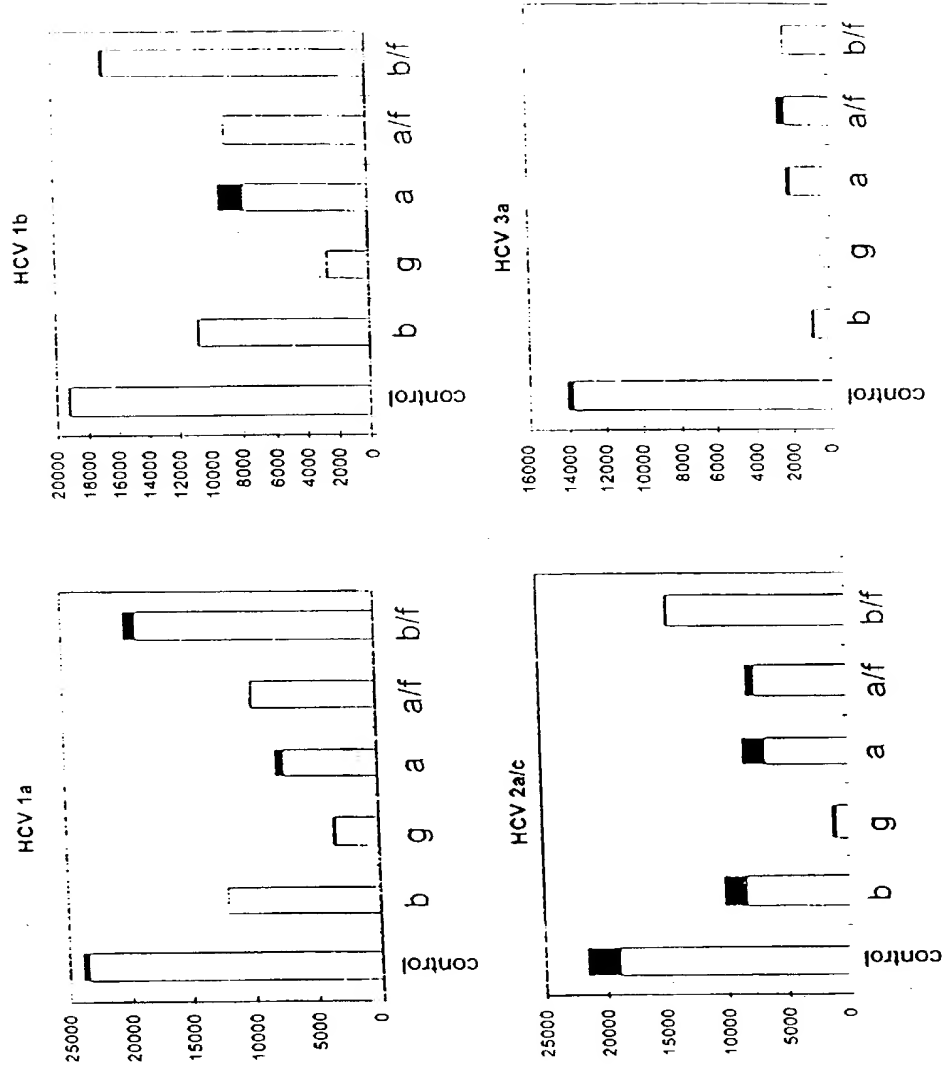
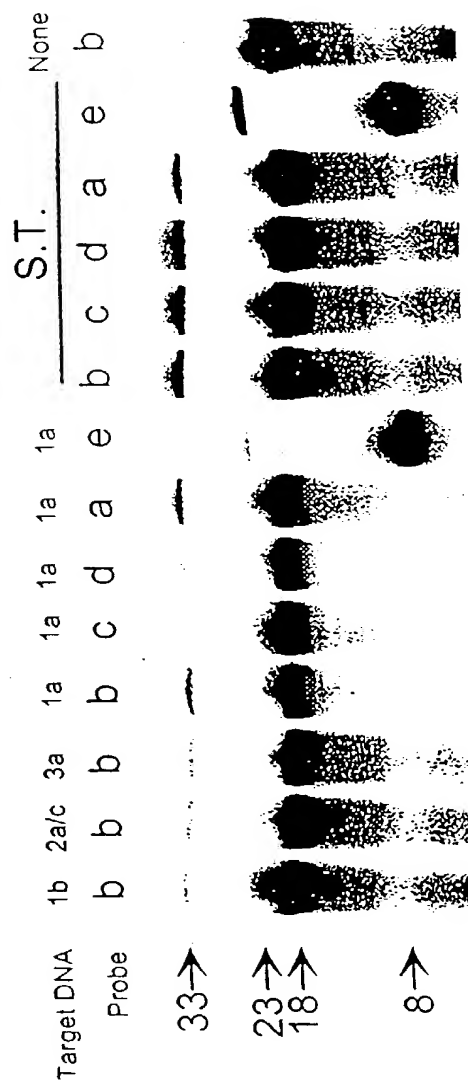


FIGURE 26

5'-ATTCCGGTGTACTCACCGGTCCAAACGACACT-3' (205-13-01) S.T.
 f (192-96-01) 3'-TAAGGCCACATGAGT-5'
 3'-GGCCAAAGCGTCTGGTGA-F1'5' (205-13-02) a
 3'-GGCCAAAGG_{TT}TGCTGTGA---F1'5' (179-49-01) b
 3'-GGCCTAGG_{TT}TGCTGTGA---F1'5' (192-72-04) c
 3'-GGCCAAAGG_{TT}TGCAGTGA F1'5' (192-72-05) d
 3'-GGCCAAAGG-F15' (205-27-01) e

FIGURE 27



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FIGURE 28

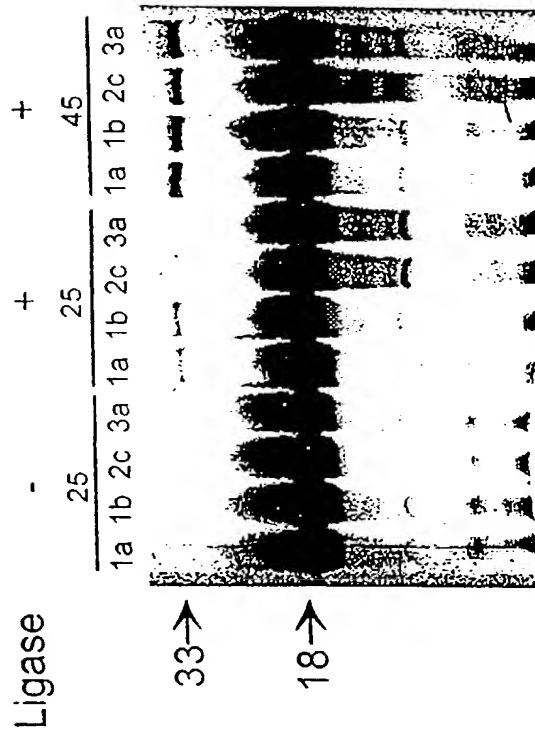


FIGURE 29A

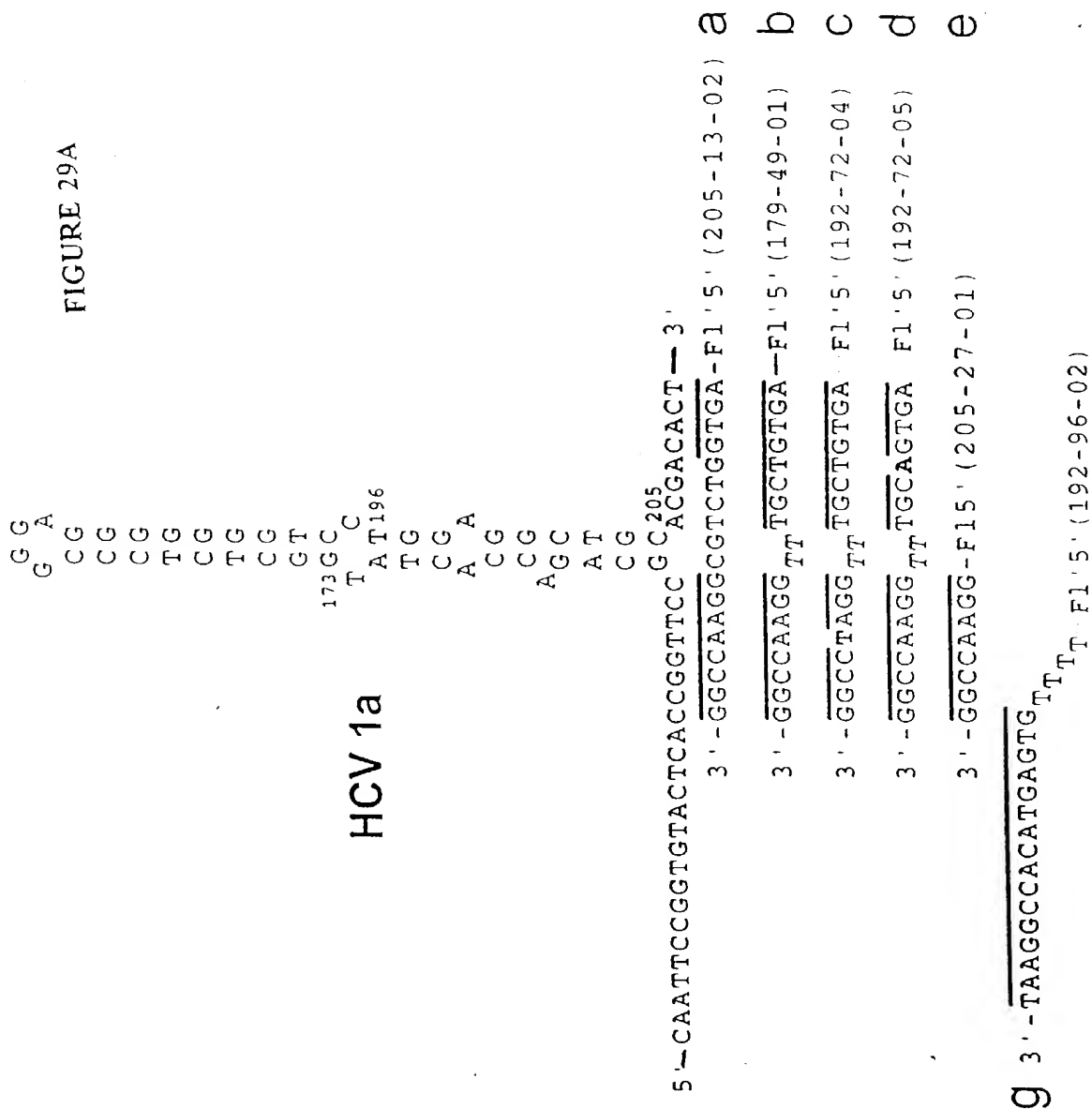


FIGURE 29B

5' -ATTCCGGTGTACTCACC GGTTCCAAACGACACT-3' (205-13-01) S.T.
 3' -GGCCAAAGCGCTCTGGTGA-F1'5' (205-13-02) a
 3' -GGCCCAAGG_{TT} TGCTGTGA--F1'5' (179-49-01) b
 3' -GGCCCTAGG_{TT} TGCTGTGA--F1'5' (192-72-04) c
 3' -GGCCCAAGG_{TT} TGCAGTGA--F1'5' (192-72-05) d
 3' -GGCCCAAGG-F15' (205-27-01) e
 g 3' -TAAGGCCACATGAGTG_{TT}
 T_T--F1'5' (192-96-02)

FIGURE 30

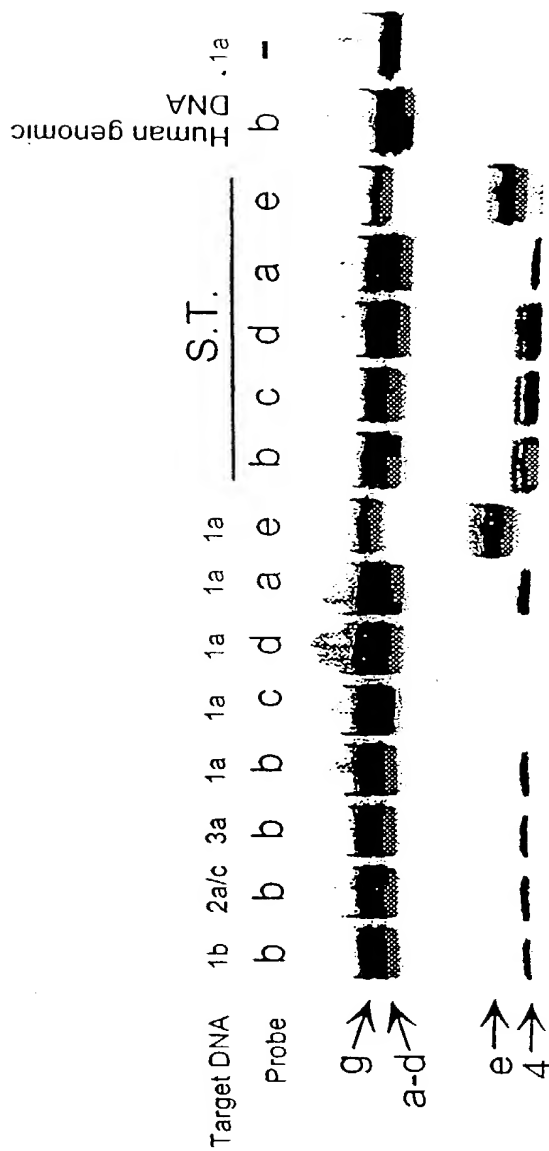


FIGURE 31

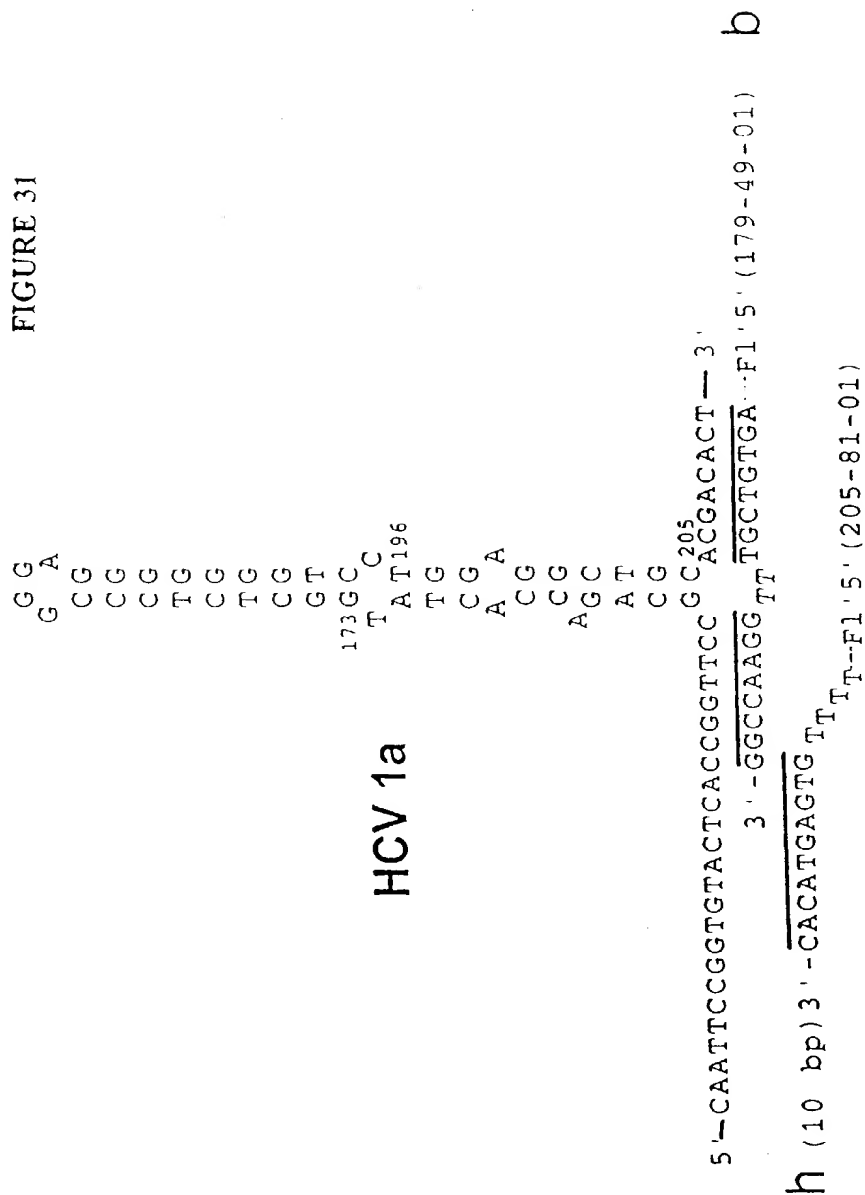
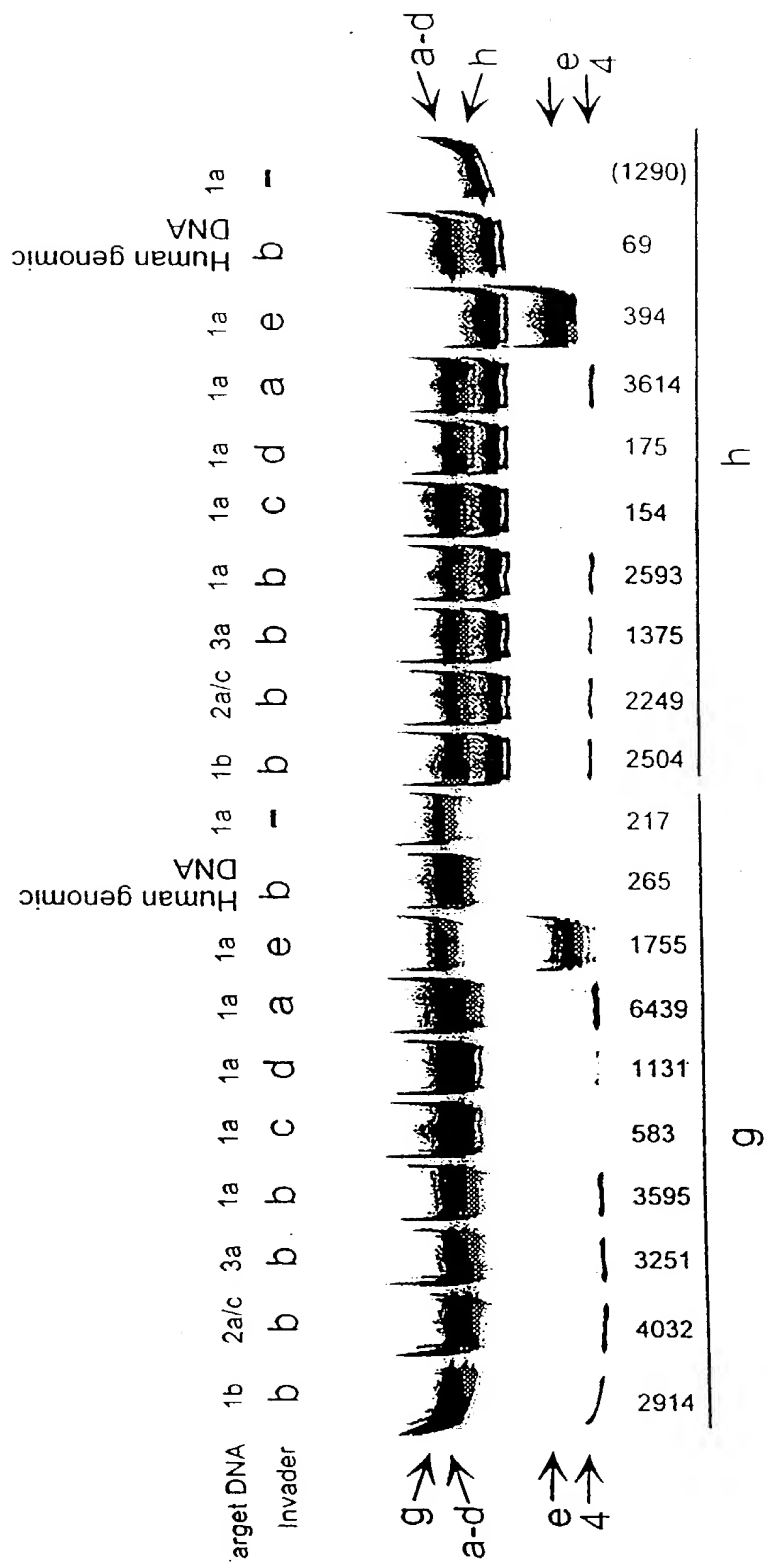


FIGURE 33

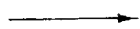


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FIGURE 34

STEPS

a



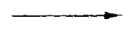
b



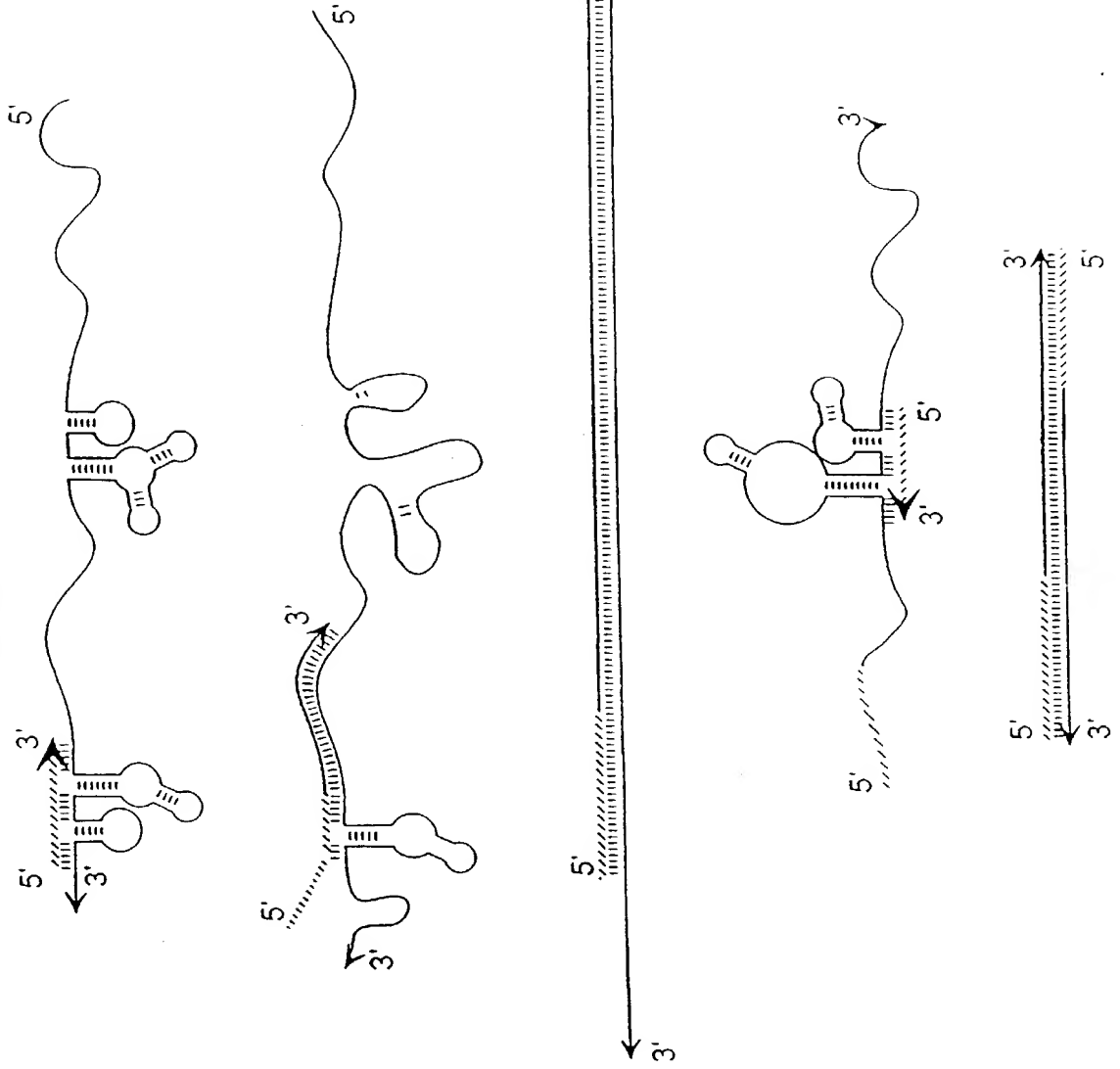
c



d



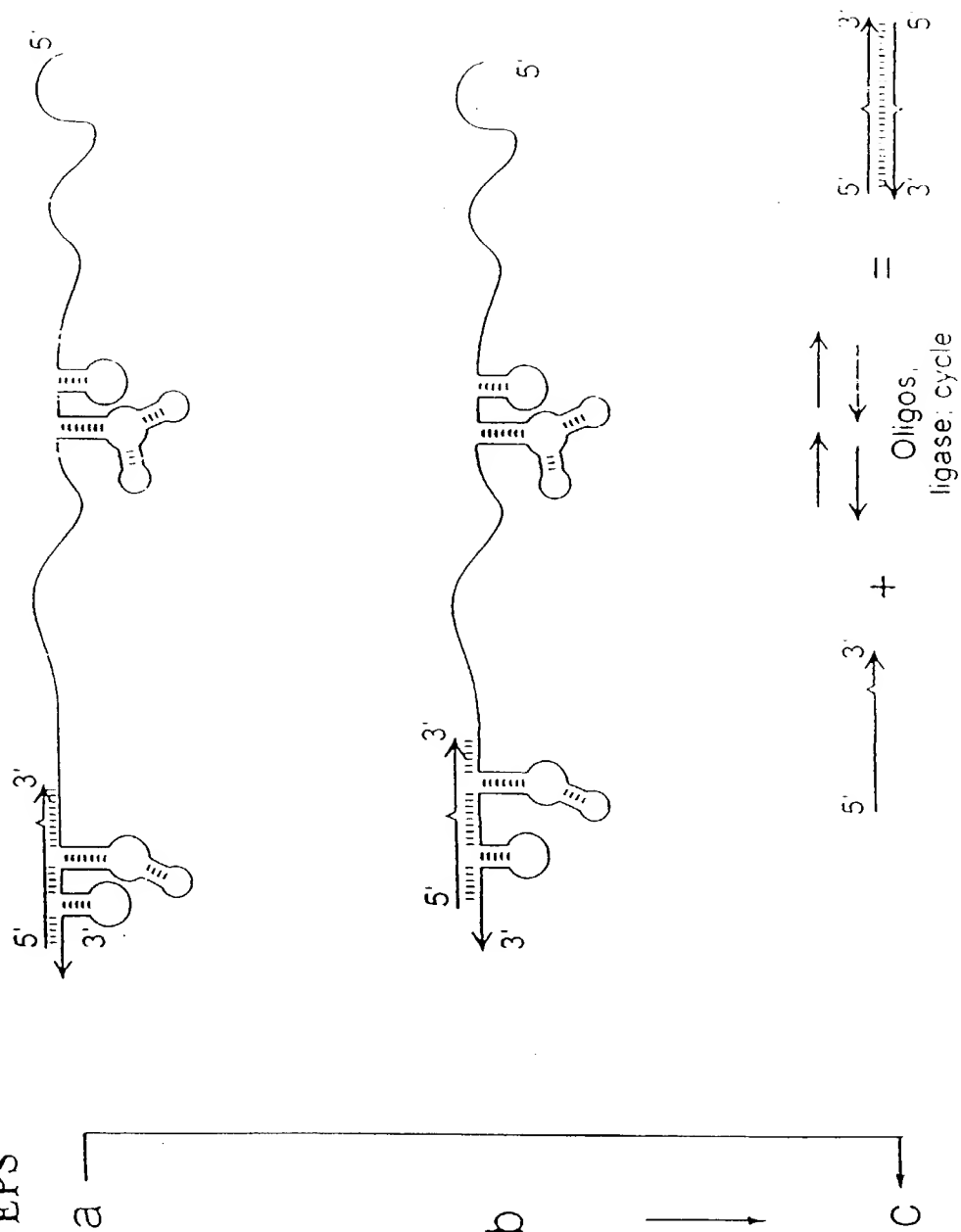
e



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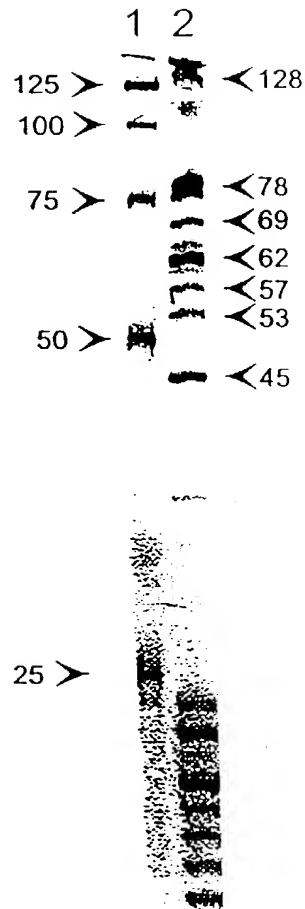
STEPS

FIGURE 35



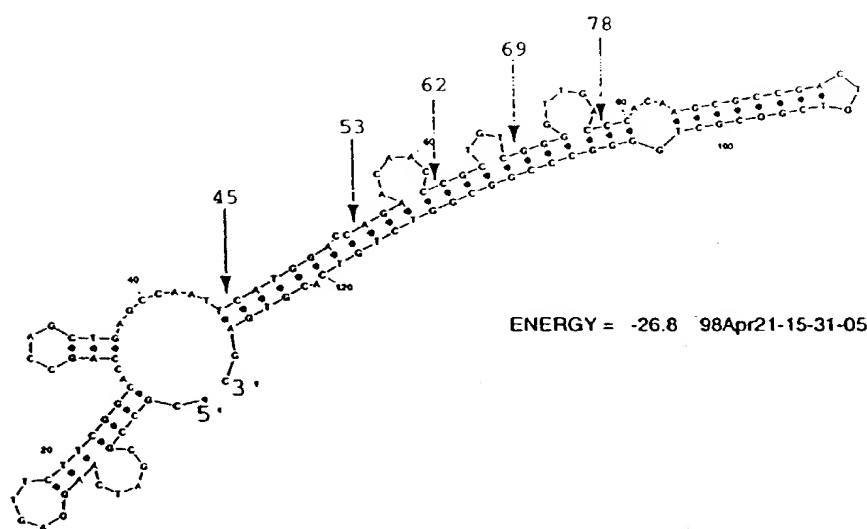
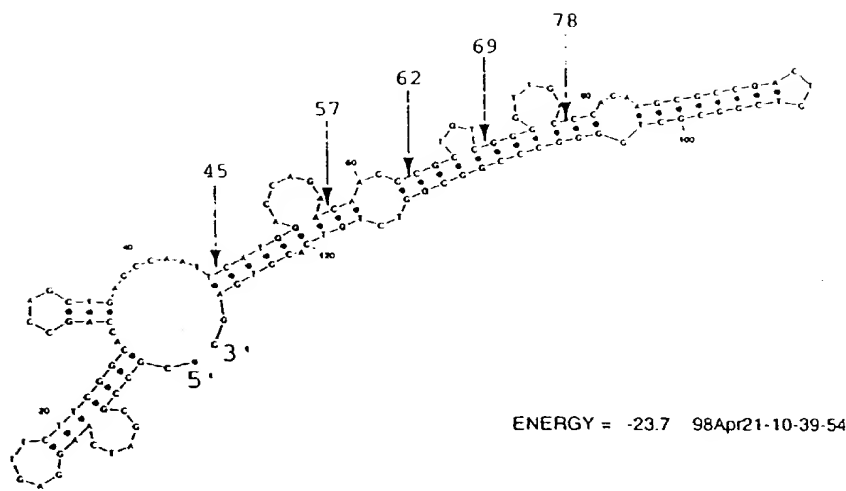
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FIGURE 36



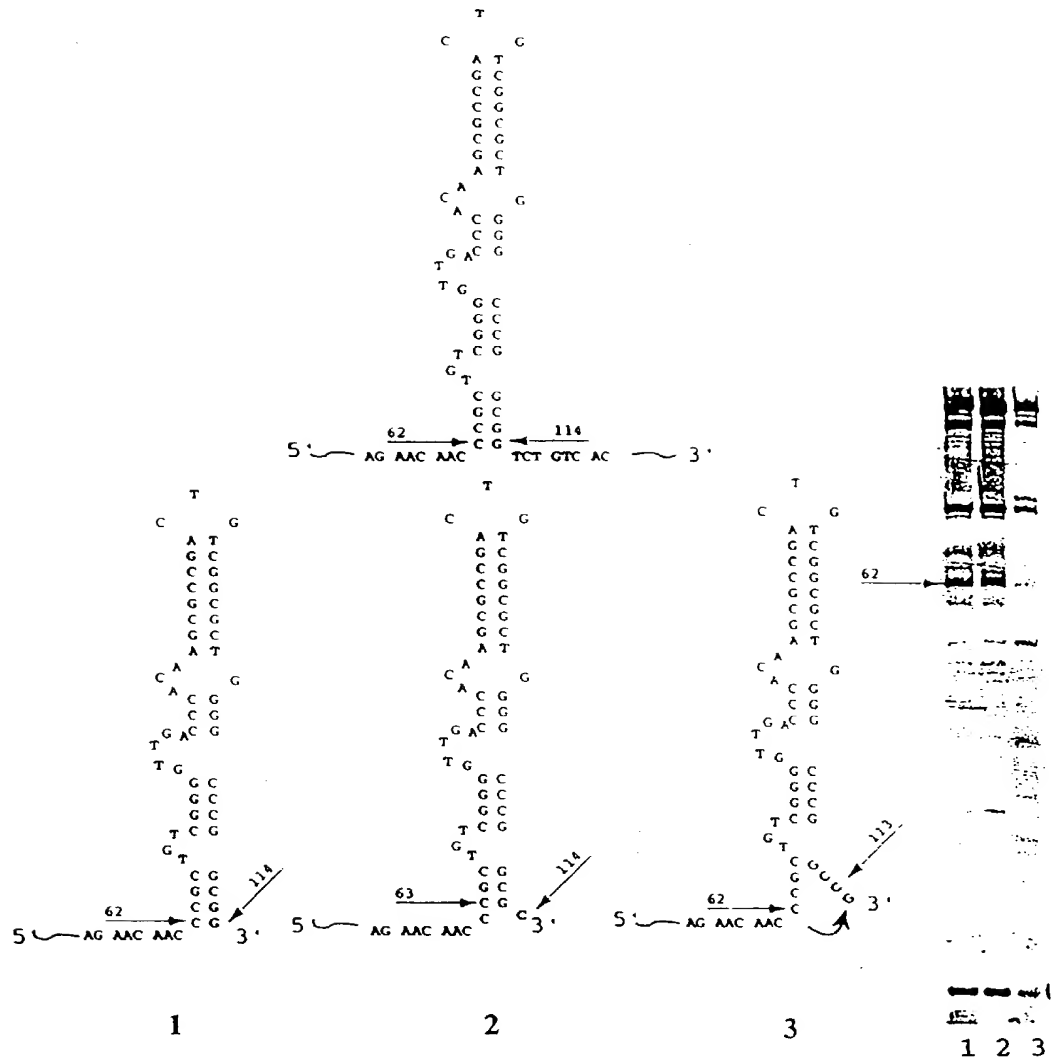
51/123

FIGURE 37A



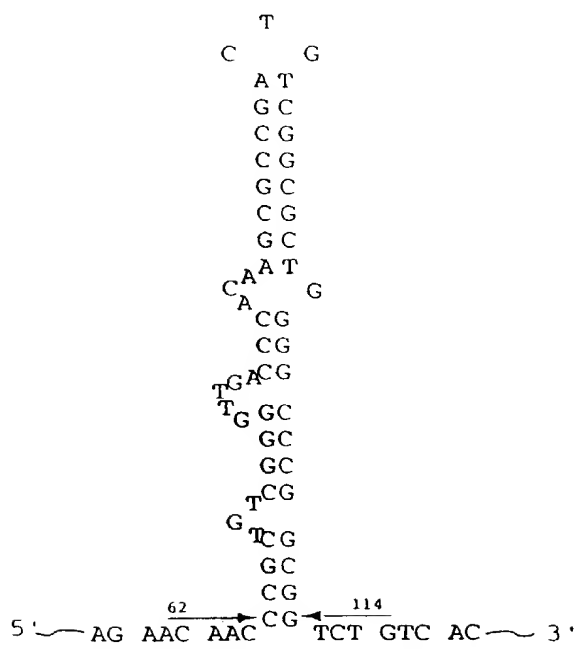
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FIGURE 37B

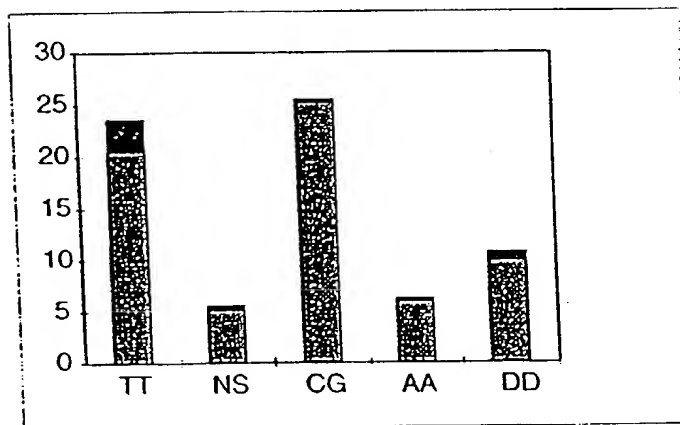


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FIGURE 37C

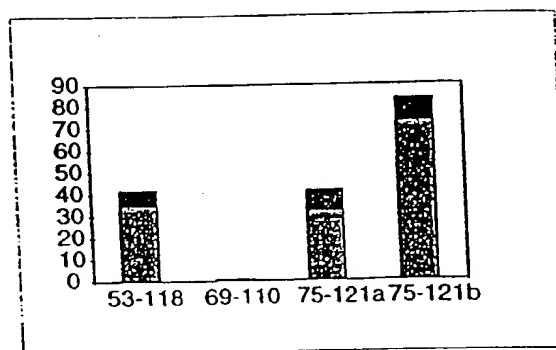
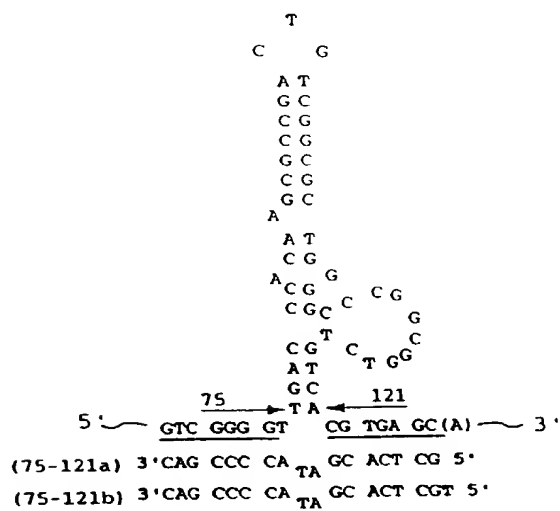
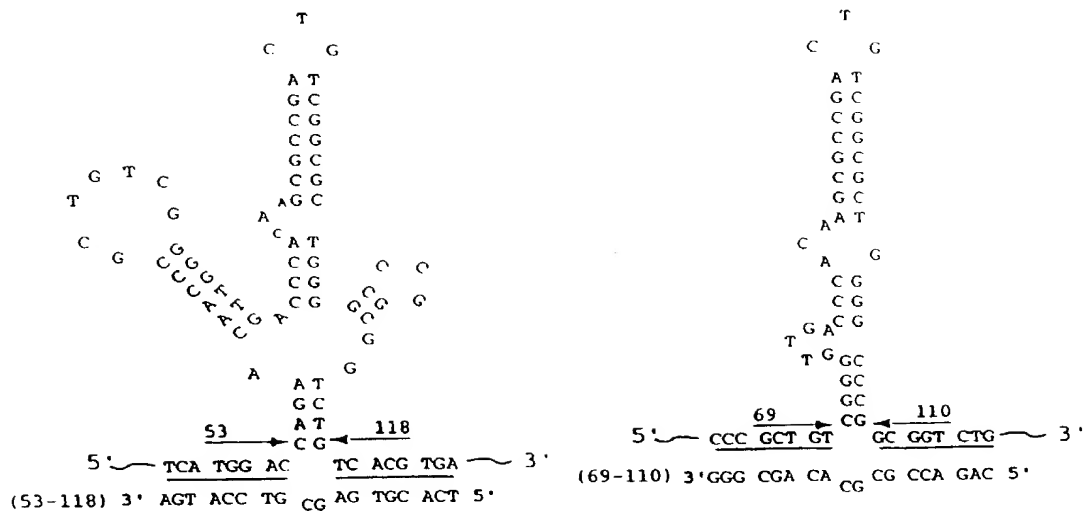


62-114 a	3' TCT TGT TG	TT	AG ACA GTG 5'
62-114 b	TCT TGT TG		AG ACA GTG
62-114 c	TCT TGT TG	CG	AG ACA GTG
62-114 d	TCT TGT TG	AA	AG ACA GTG
62-114 e	TCT TGT TG	DD	AG ACA GTG



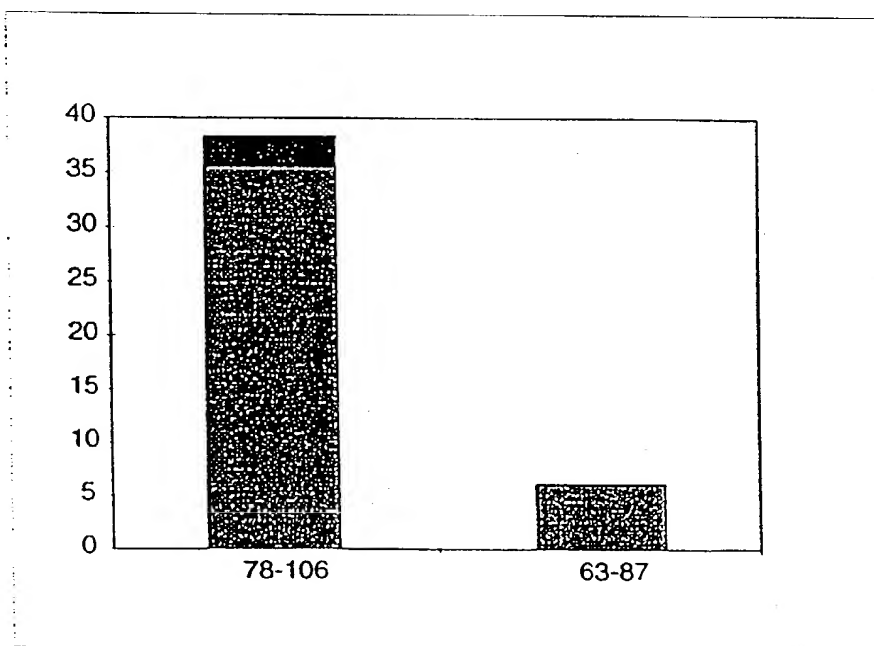
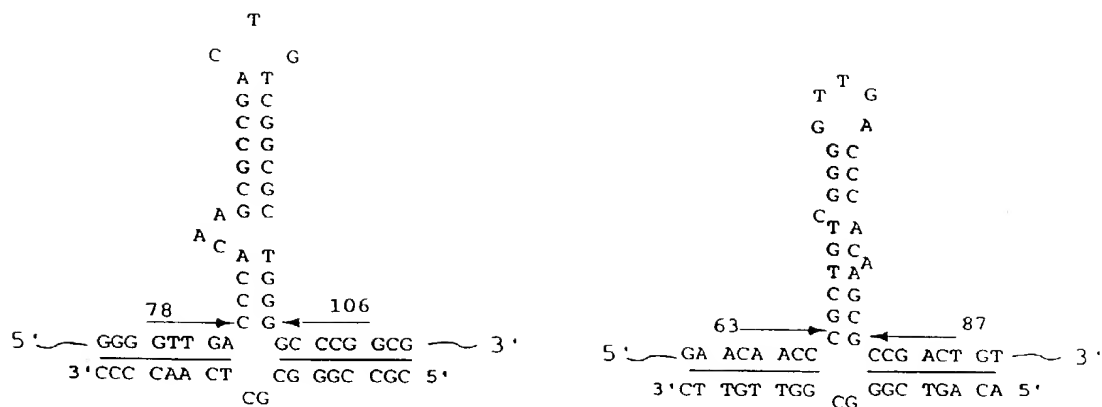
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FIGURE 38A



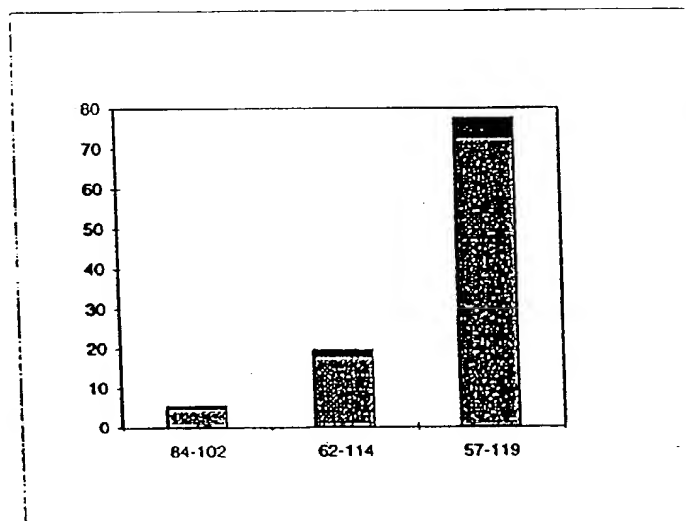
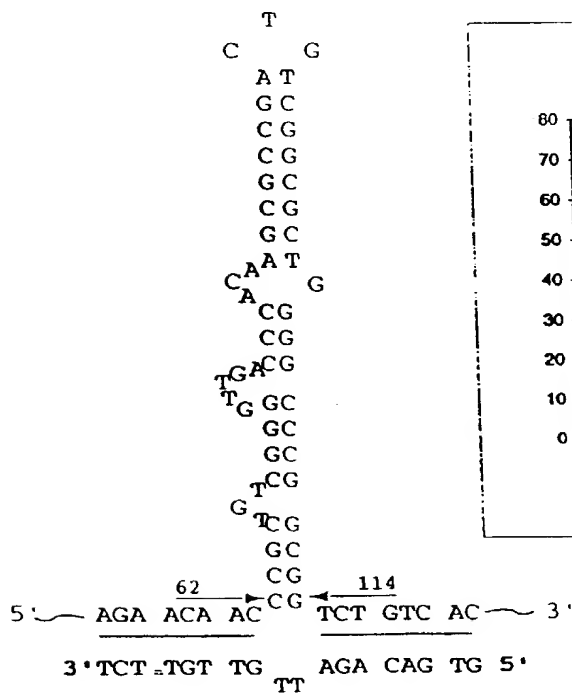
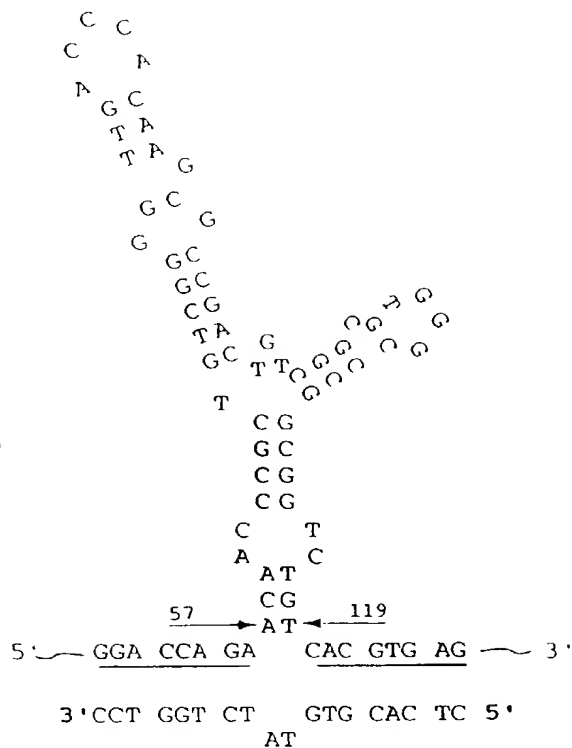
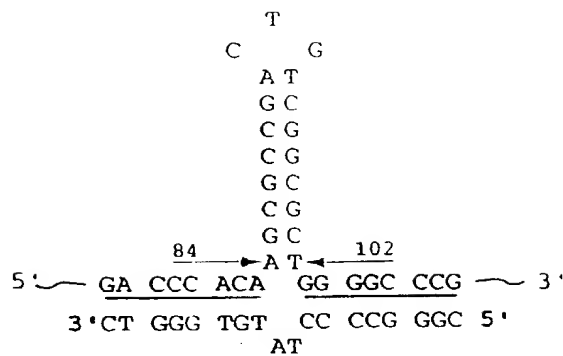
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FIGURE 38B



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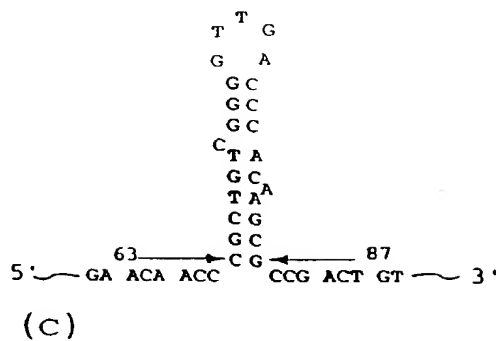
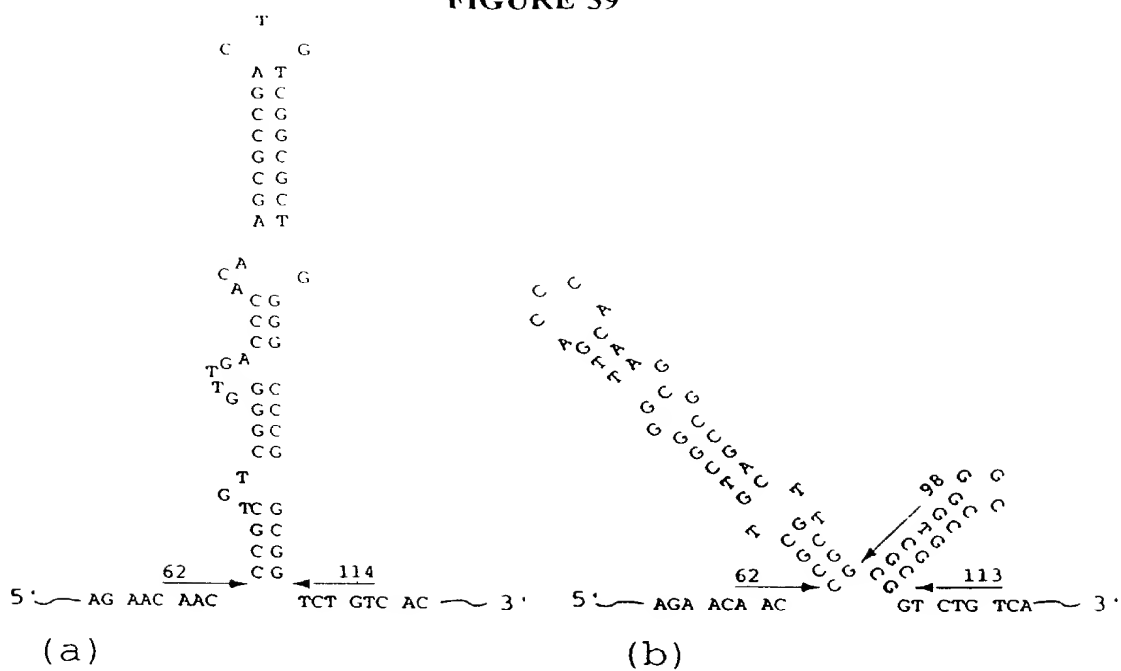
FIGURE 38C



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09882945-061501

FIGURE 39



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Physical characteristics		Chemical composition		Mechanical properties		Thermal properties		Electrical properties	
Parameter	Value	Parameter	Value	Parameter	Value	Parameter	Value	Parameter	Value
Length	100 mm	Carbon content	0.25%	Tensile strength	550 MPa	Softening point	2800 °C	Volume resistivity	10 ¹² Ω·cm
Width	10 mm	Sulfur content	0.005%	Elongation at break	15%	Thermal conductivity	15 W/m·K	Surface resistivity	10 ¹¹ Ω/sq
Thickness	2 mm	Phosphorus content	0.01%	Yield strength	350 MPa	Thermal expansion coefficient	12 × 10 ⁻⁶ /°C	Dielectric constant	3.5
Weight	20 g	Manganese content	0.03%	Impact strength	10 J/m²	Thermal stability	2000 h at 1000 °C	Dielectric loss tangent	0.02
Color	Gray	Silicon content	0.02%	Hardness	180 HB	Thermal shock resistance	100 °C/min	Thermal aging	1000 h at 150 °C
Surface finish	Polished	Copper content	0.01%	Weldability	Good	Thermal fatigue	100 cycles	Thermal conductivity	15 W/m·K
Texture	Smooth	Nickel content	0.01%	Corrosion resistance	Good	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Aluminum content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Chromium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain orientation	Random	Vanadium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain shape	Equiaxed	Niobium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Antimony content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Strontium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain orientation	Random	Barium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain shape	Equiaxed	Calcium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Magnesium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Zinc content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain orientation	Random	Aluminum content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain shape	Equiaxed	Chromium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Vanadium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Niobium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain orientation	Random	Antimony content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain shape	Equiaxed	Strontium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Barium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Calcium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain orientation	Random	Magnesium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain shape	Equiaxed	Zinc content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Aluminum content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Chromium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain orientation	Random	Vanadium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain shape	Equiaxed	Niobium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Antimony content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Strontium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain orientation	Random	Barium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain shape	Equiaxed	Calcium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain size	0.5 μm	Magnesium content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K
Grain boundary	Clear	Zinc content	0.01%	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K	Thermal conductivity	15 W/m·K

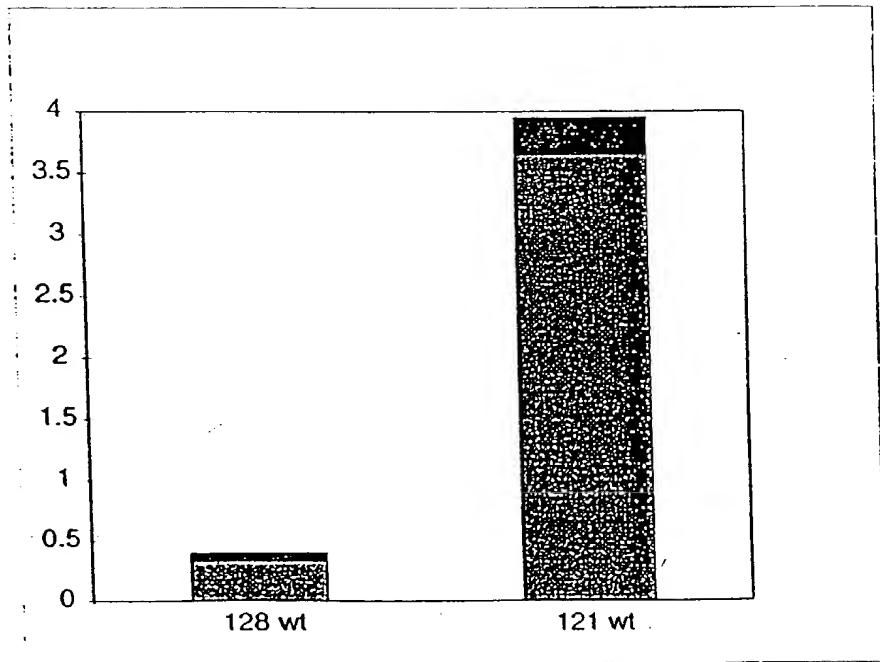
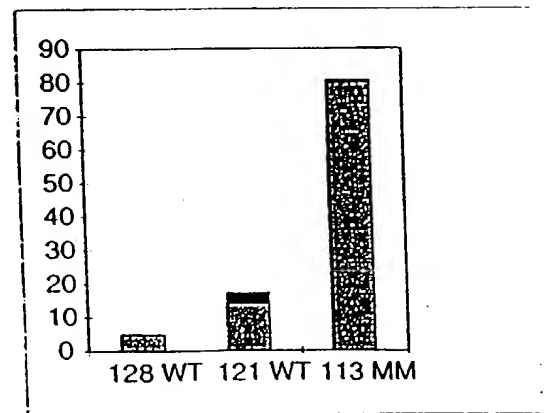
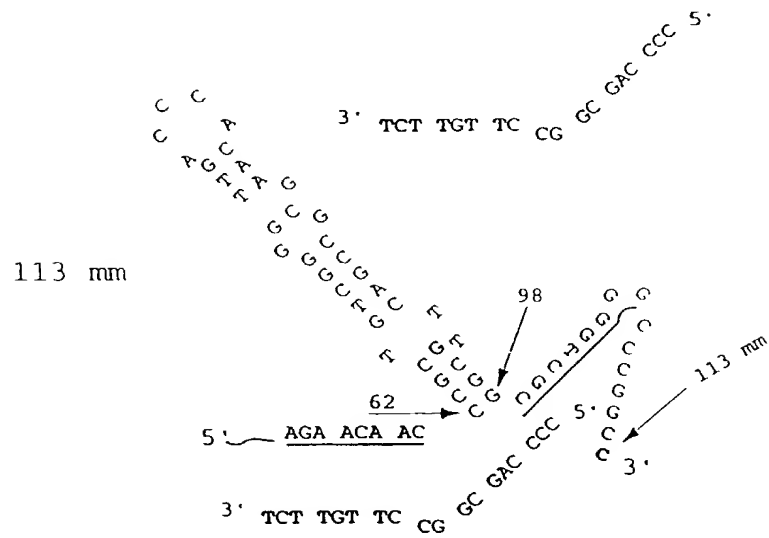
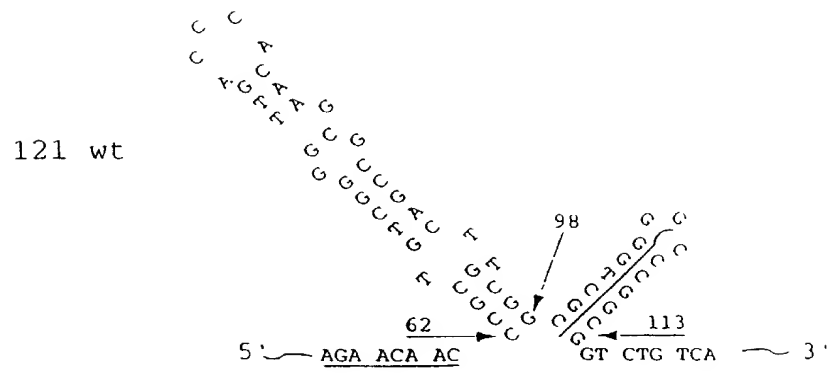
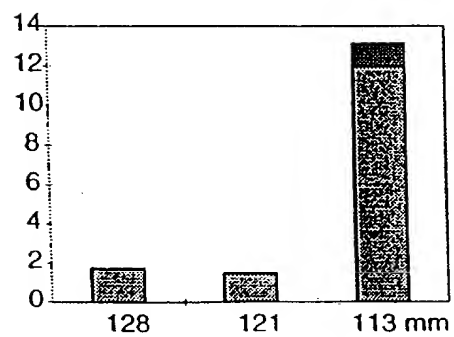
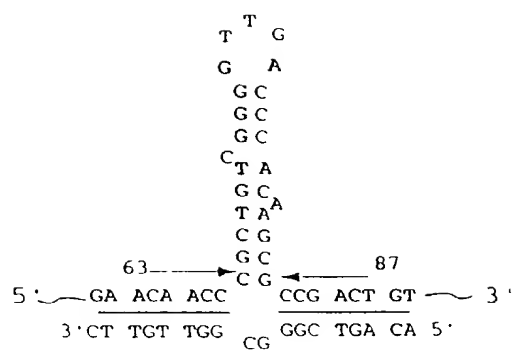

$$\frac{59}{123}$$

FIGURE 41



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FIGURE 42



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FIGURE 43A

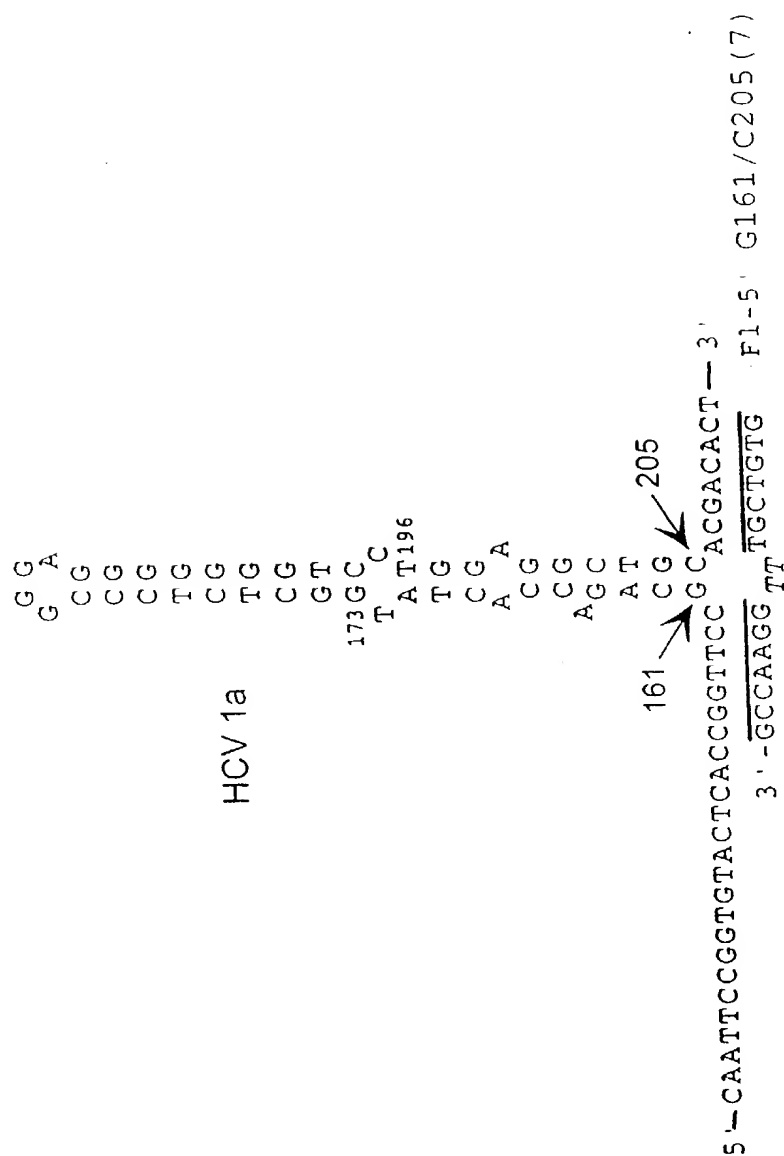
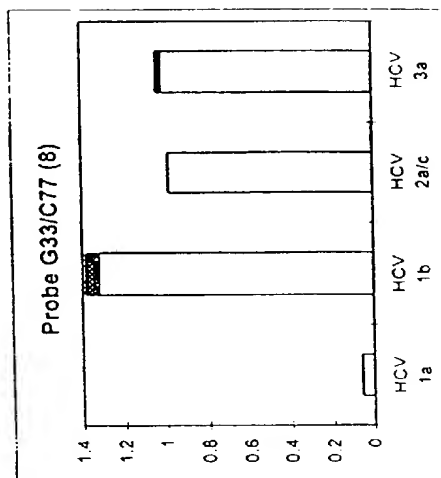


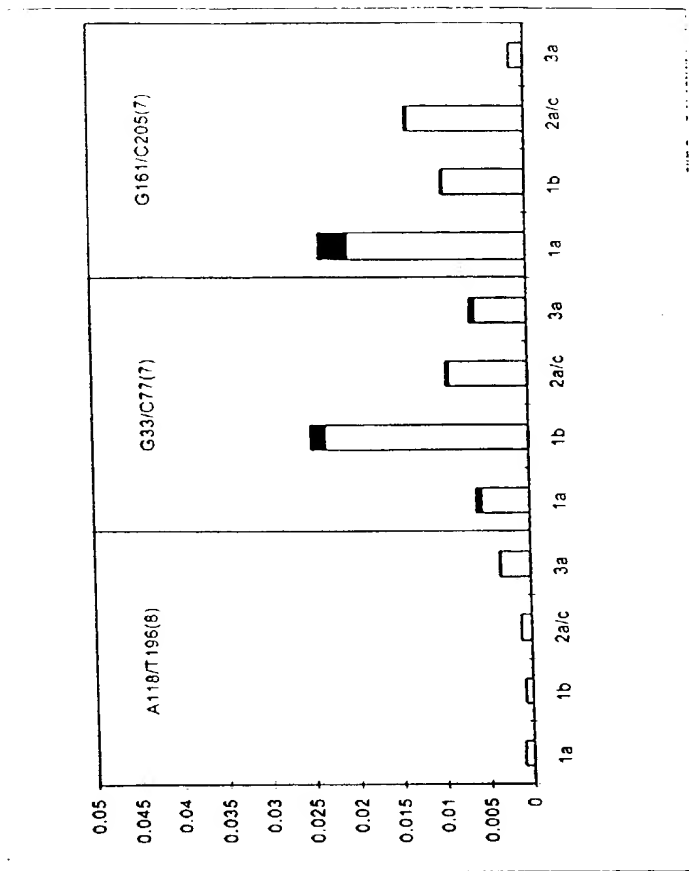
FIGURE 44A



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TESTED " 54533860

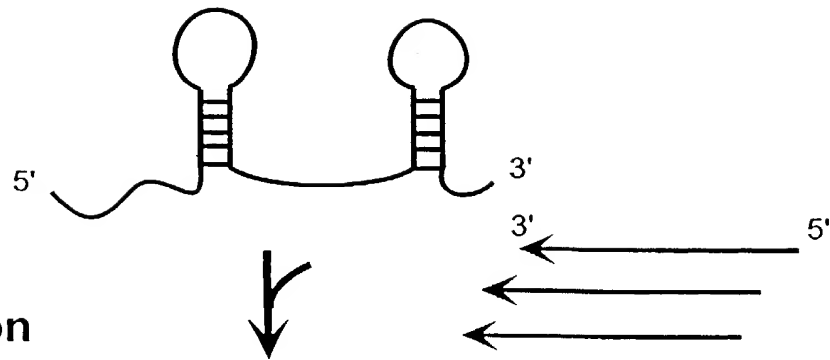
FIGURE 44B



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0982945 061501
POSTNET 51628860

I) Hybridization



II) Reverse Transcription

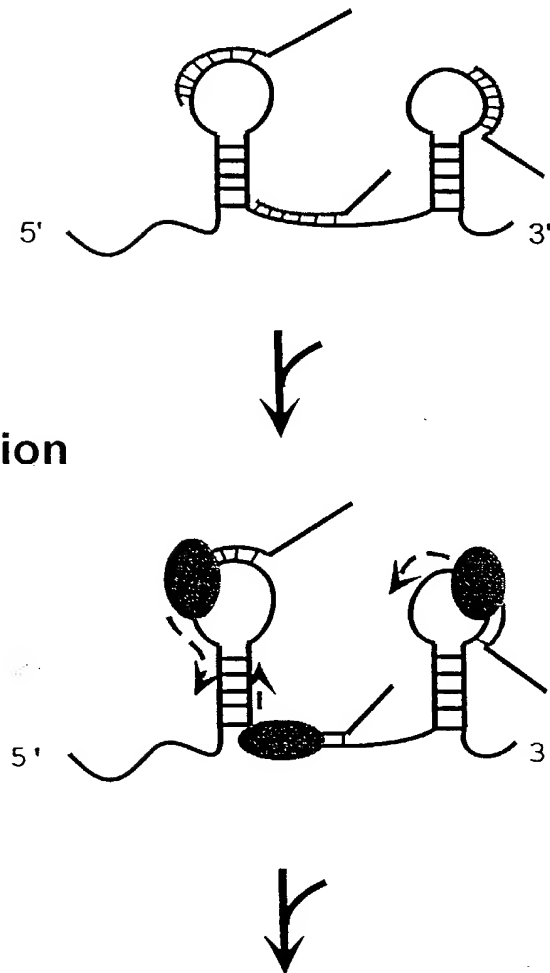
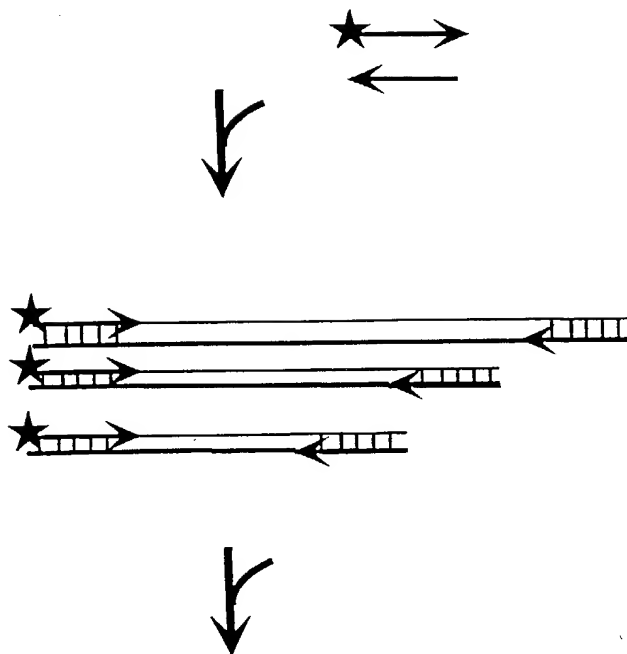


FIGURE 45A

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0982915 061501
TOST90" SH628860

III) PCR



IV) PAGE with Sequencing Ladder

A C G T RT-Products

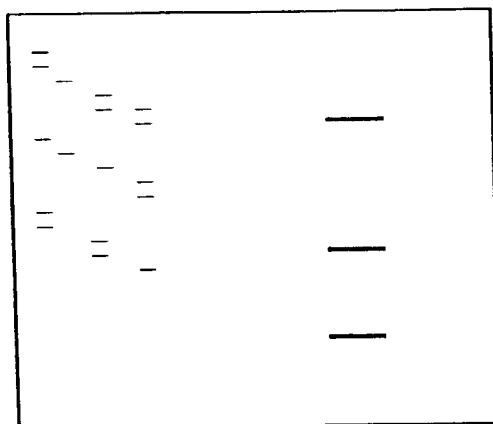
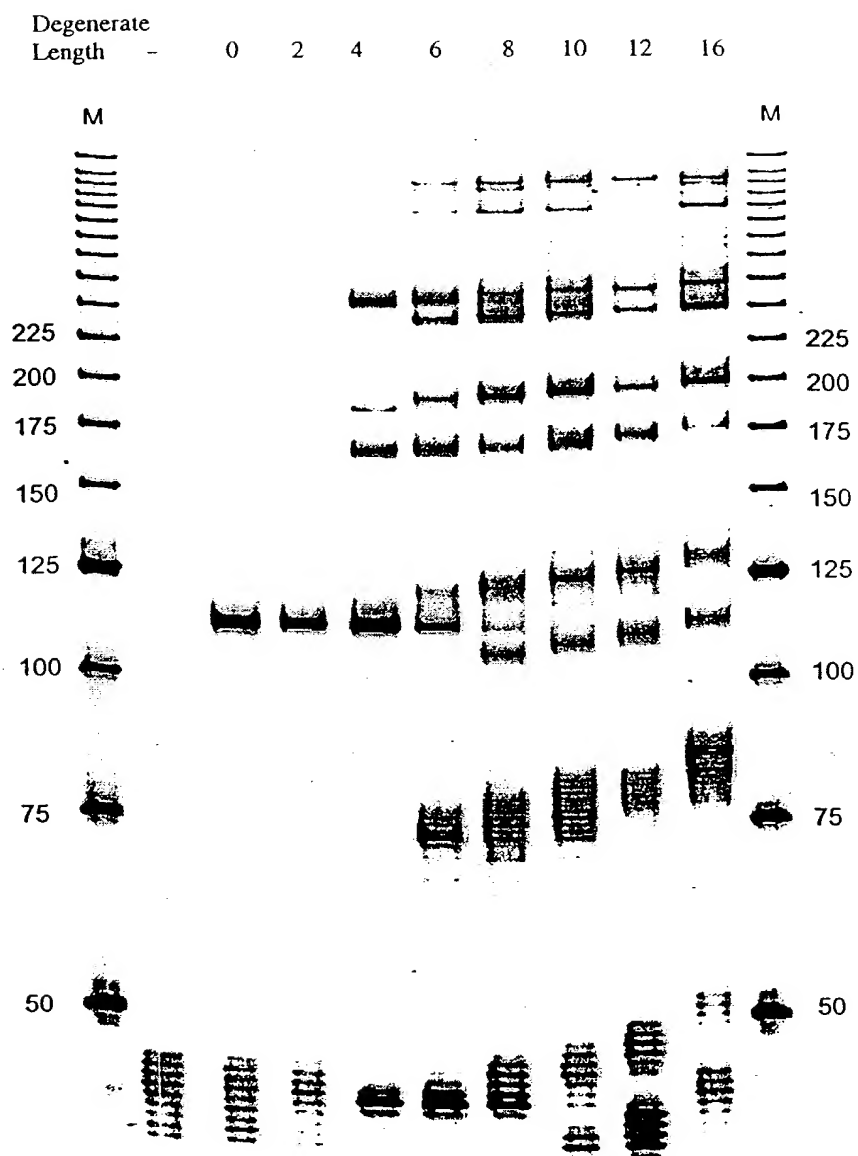


FIGURE 45B

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FIGURE 46



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09882945-061501

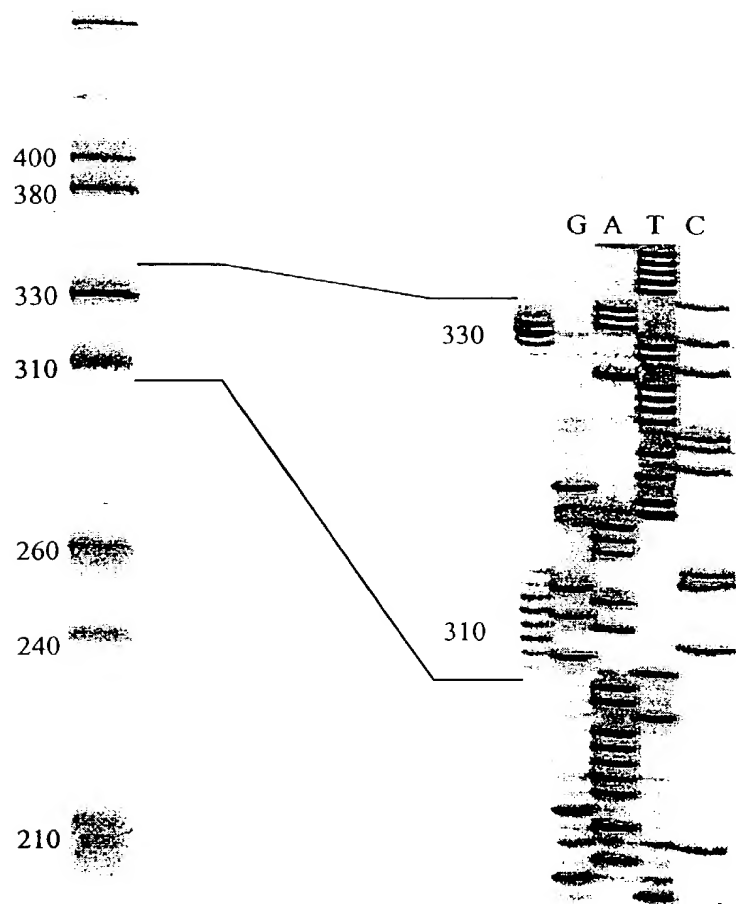


FIGURE 47

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105F90" 54628860

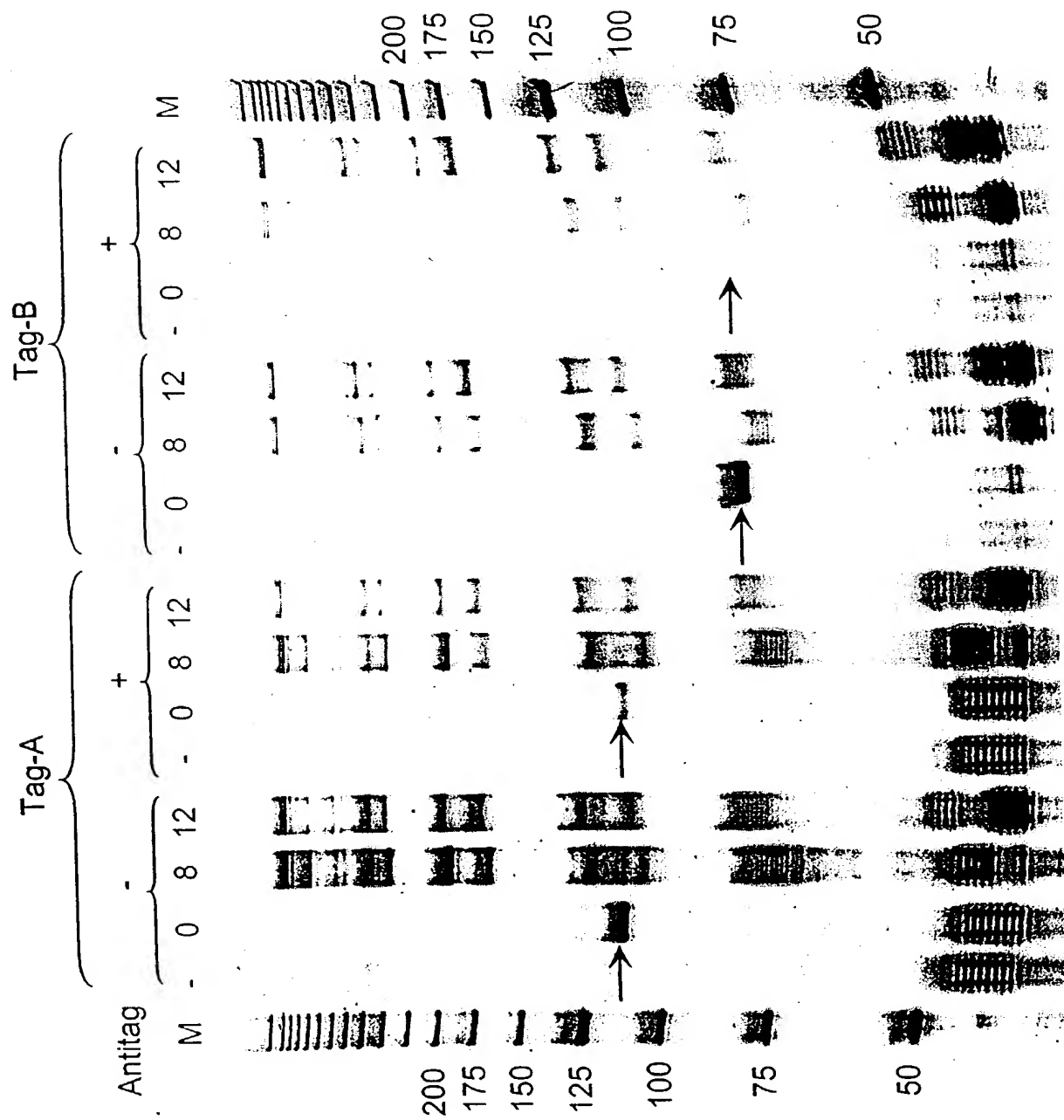


FIGURE 48

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09882945.064501

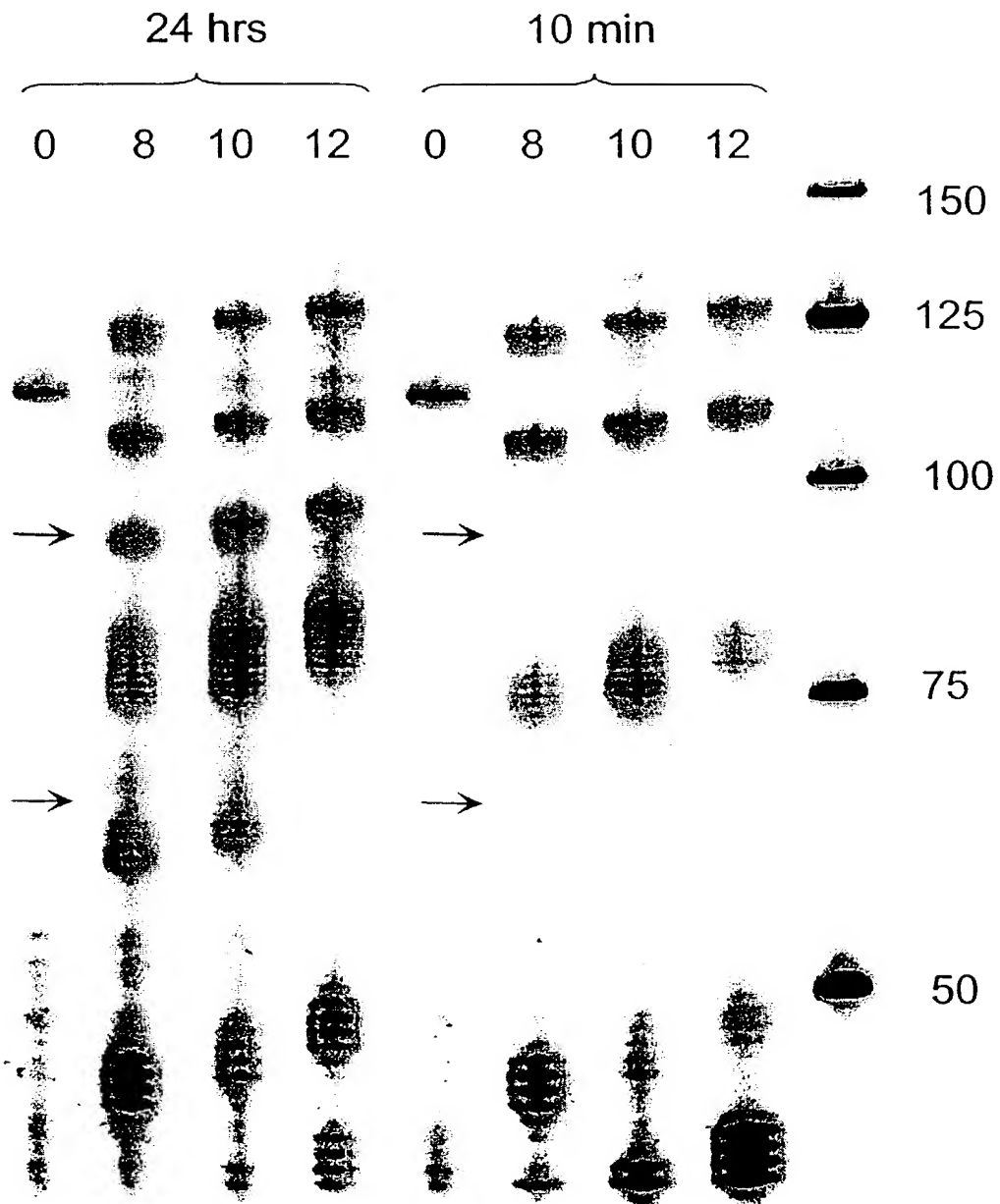
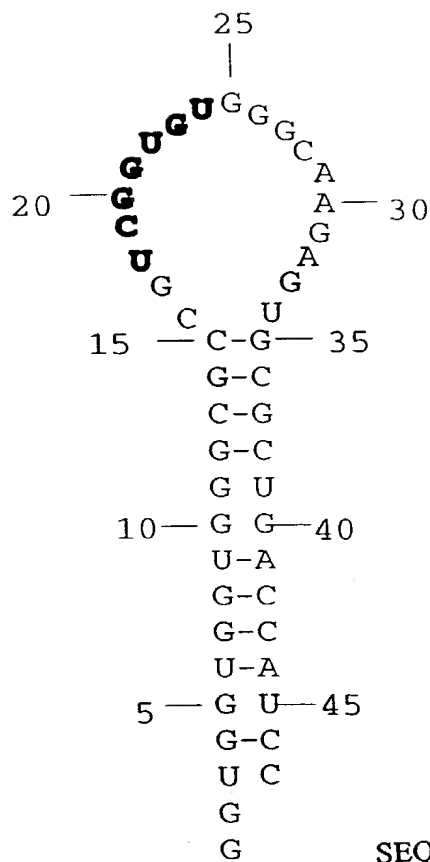


FIGURE 49

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09882945.06.150.1



SEQ ID 142

FIGURE 50A

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0988245-04501
T05T90-54628860

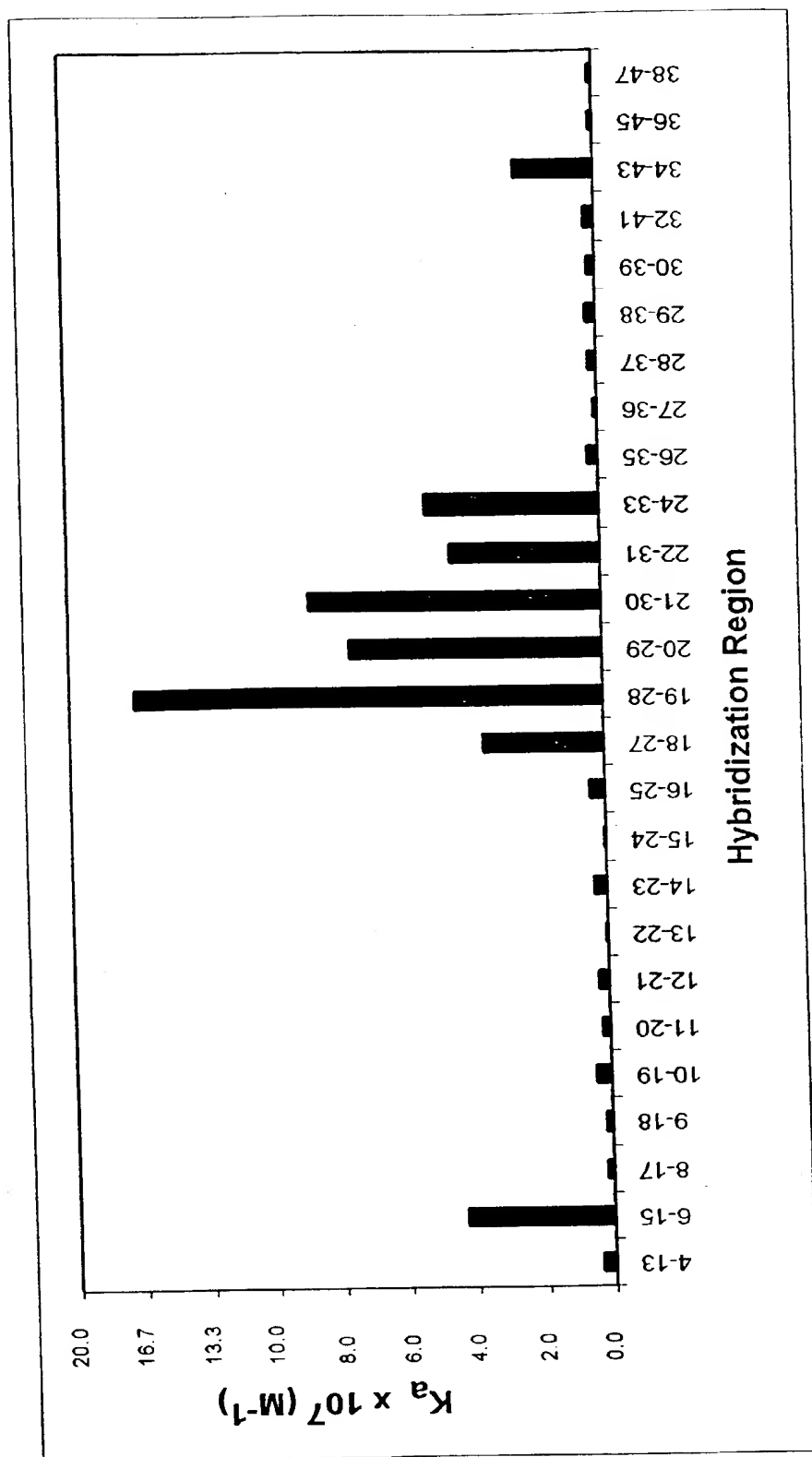


FIGURE 50B

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FIGURE 51

1 ACACUUGCUU UUGACACAAC UGUGUUUACU UGCA**AAUCCCC** CAAAACAGAC

51 AGA**AUGGUGC** AUCUGUCCAG UGAGGAGA**AAG** **UCUGCGGUCA** CUGCCCUGUG

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

09662945.061501

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FIGURE 52A

ISIS 1571(-) ISIS 3067(+)

1 GCGCCCC AGT CGACGCTGAG CTCCT CTGCT ACTCAGAGTT

ISIS 1570(+)

41 GCAACCTCAG CCTCGCTATG GCTCCCAGCA GCCCCCGGCC

81 CGCGCTGCCC GCACTCCTGG TCCTGCTCGG GGCTCTGTTC

121 CCAGGACCTG GCAATGCCCA GACATCTGTG TCCCCCTCAA

161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG

201 CAGCACCTCC TGTGACCAGC CCAAGTTGTT GGGCATAGAG

241 ACCCCGTTGC CTAAAAAGGA GTTGCTCCTG CCTGGGAACA

281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934(-)

321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA

361 ACAGCTAAAA CCTTCCTCAC CGTGTACTGG ACTCCAGAAC

401 GGGTGGA ACT GGCACCCCTC CCCTCTTGGC AGCCAGTGGG

441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGGCA

481 CCCCGGGCCA ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

0986245-061501

75/
123

FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA

as 610

561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA

601 GCCAATTTCT **CGTGCCGCAC** TGA ACTGGAC CTGCGGCCCC

641 AAGGG**CTGGA** GCTGTTTGAG AAC**ACCTCGG** CCCCCTACCA

681 GCTCCAGACC TTTGTC**TGC** **CAGCGACTCC** CCCACA ACTT

721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG

761 TGGTCTGTTC CCT**GGACGGG** CTGTTCCCAG TCT**CGGAGGC**

801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC

841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT

881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT

921 GACGTGTGCA GTAATACTGG GGAACCAGAG **CCAGGAGACA**

961 CTGCAGACAG **TGACCATCTA** CAGCTTTCCG GCGCCCAACG

1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

09022945-061501

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11. JRE 52C

1041 GACAGTGAAG TGT**GAGGCCC** ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGGCGCAG**

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG GGAGCTTCGT GTCCTGTAT**G**

1241 **GCCCCCGACT** GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGGCCAGAA AATT**CCCAGC** AGACTCCAAT GTGCCAGGCT

1321 TGGGGGAACC CATTGCCCGA GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTTT**CCC** ACTGCCCATC **GGGGAATCAG** TGA**CTGTCAC**

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGT**CG** GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGGCA** CTGCAGGCCT **CAGCACGTAC**

0988945.061501

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FIGURE 52D

1561 CTCTATAACC GCCAGCGGAA GATCAAGAAA TACAGACTAC

as 1630 as 1630h(+++)

1601 AACAGGCCCA AAAAGGGACC CCCATGAAAC CGAACACACA

ISIS 1938 (+)

1641 AGCCACGCCT CCCTGAACCT ATCCCGGGAC AGGGCCTCTT

1681 CCTCGGCCTT CCCATATTGG TGGCAGTGGT GCCACACTGA

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCTACCGG

1761 CCCTGGGACG CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 TACAACAGCA TTTGGGGCCA TGGTACCTGC ACACCTAAAA

1841 CACTAGGCCA CGCATCTGAT CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGAAG GAGCAAGACT CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGATGAG AGGGGAAGTG GTGGGGGAGA

1961 CATAGCCCCA CCATGAGGAC ATACAACTGG GAAATACTGA

2001 AACTTGCTGC CTATTGGGTA TGCTGAGGCC CACAGACTTA

2041 CAGAAGAAGT GGCCCTCCAT AGACATGTGT AGCATCAAAA

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URE 52E

ISIS 2302 (+)

2081 CACAAAGGCC CACACTTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA CTGACCCCAA CCCTTGATGA TATGTATTTA

ISIS 1572

2161 TTCATTTGTT ATTTTACCAG CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT ACACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CAAATGGGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTTC TATCGGCACA AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGGTTCAAGAG ATTACCCAGT

2441 GAGGCCTTAT TCCTCCCTTC CCCCCAAAAC TGACACCTTT

2481 GTTAGCCACC TCCCCACCCA CATACATTTTC TGCCAGTGTT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGAATATG CCCAAGCTAT GCCTTGTCTCT CTTGTCCTGT

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URE 52F

2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

0982945-061501

80/123

0986345-064501

81/123

III 53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG

site 560

521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC

site 570

561 AGCAGCUAAA ACAGGGAAGC GAAAAAGGAG UCAGAUGCUG

601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC

641 UACAAUAUUU GAAUUUUAAA UCUAAAUCUA UUUUAUAAUA

681 UUUAACAUIA UUUUAUAUGGG GAAUAUAUUU UUAGACUCAU

721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG

761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUUA UUAUAAUCC

801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA

site 850

site 860

site 880

841 CUAUUUAGGC AAGGCUAUGU GAUUACAAGG CUUUAUCUCA

site 890

site 910

881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG

921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUUAU

961 AAGUGAAGUG AUACUAUCCA GUUACUA

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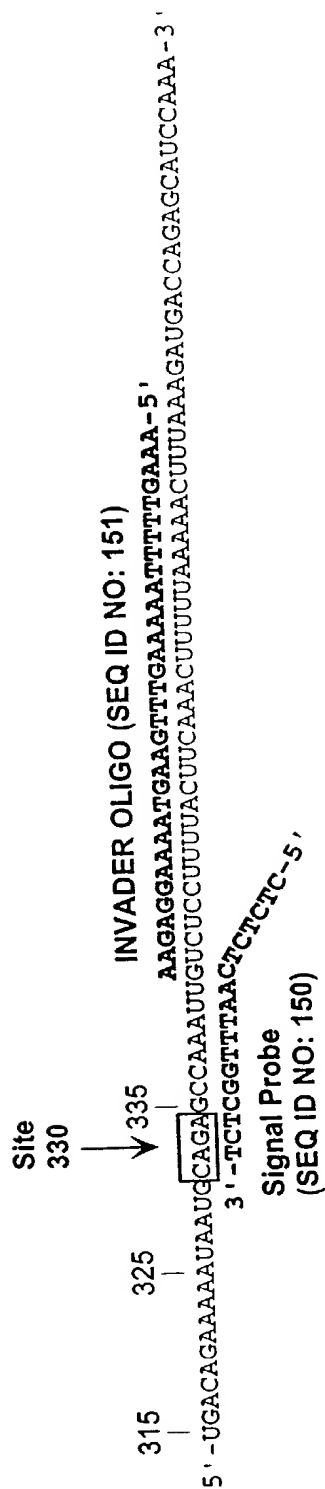
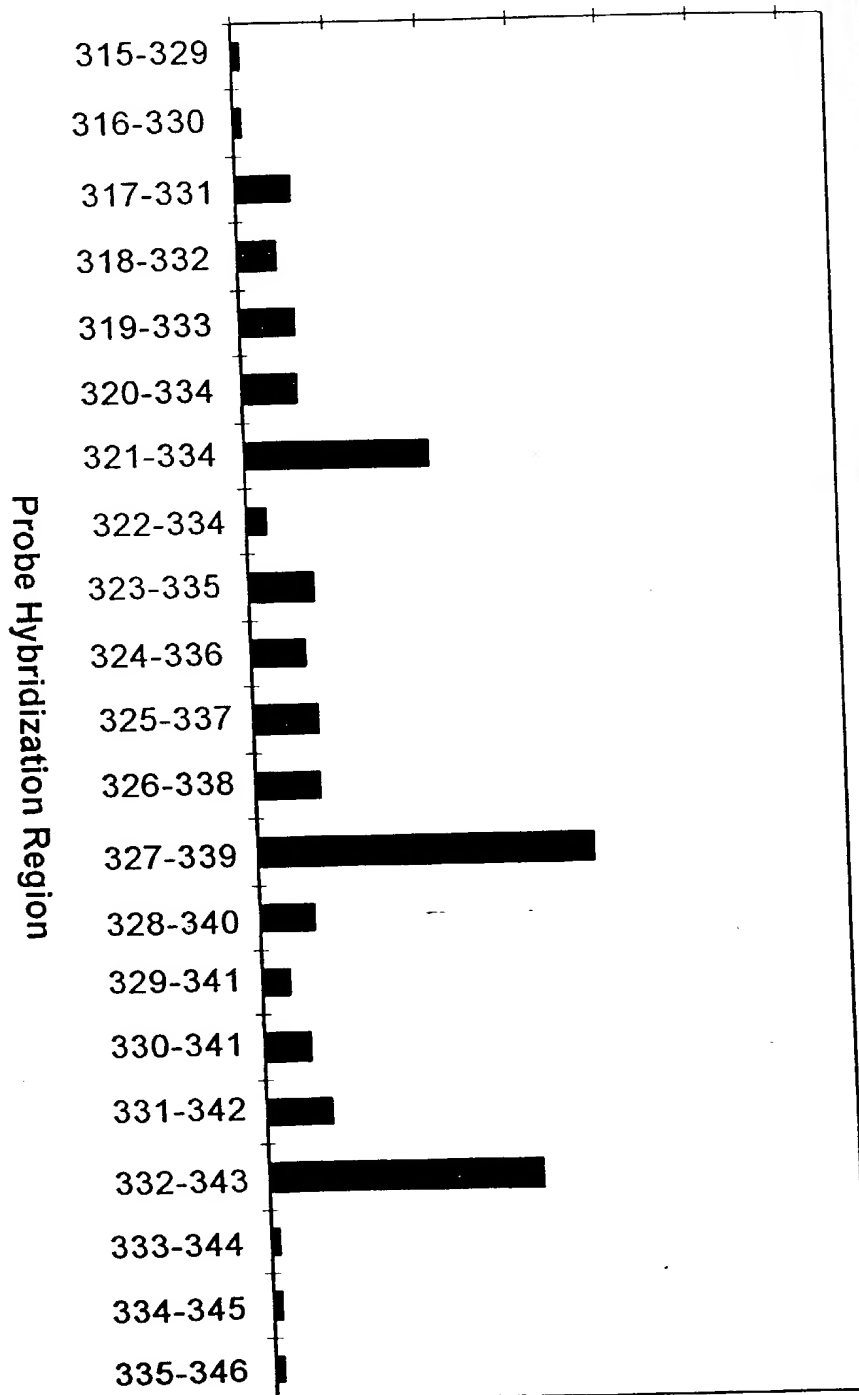


FIGURE 54A

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Turnover Rate (min^{-1})

0 1 2 3 4 5 6



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FIGURE 54B
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FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUA GCGGGGGAGA AUUAGAUCGA UGGGAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUUAAA ACAUUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUAGAA

960 GGCUGUAGAC AAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC

Primer 4

1010 AGAAGAACUU AGAUCAUUU AUAAUACAGU AGCAACCCUC UAUUGUGUGC

1060 AUCAAAGGAU AGAGAUAAAA GAC**CCAAGG** AAGCUUUAGA CAAGAU**AGAG**

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FIGURE 55B

1110 **GAA**GAGCAAA ACAAAGUAA GAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGG**ACACAGC AAUCAGGUCA GCCAAAUUA CCCUAUAGUG CAGAACAUC

Primer 5

1210 **AGGGG**CAAAU GGUACAUCAG GCCAUAUCAC CUAGAACUUU AAAUGCAUGG

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU

1310 UUCAGCAUUA UCAGAA**GGAG** **CC**ACCCACACA AGAUUUAAAC ACCAUGC

1360 ACACAGUGGG GGGACAUC**AA** **GC**AGCCAUGC AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAUG**AGGAAG CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGC**ACCA** GGCCAGAUGA GAGA**ACCAAG** **GG**GAAGUGAC AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCAGUAG GAGAAAUUUA UAAAGAUGG AUAAUCCUGG GAUUAUUAA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAU AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCC**GAGCAAG CUUC**ACAGGA** GGUAAAAAU **UGG**AUGACAG AAACCUUGUU

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[illegible]

Primer 8

1860 CCCGGCCAUA AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

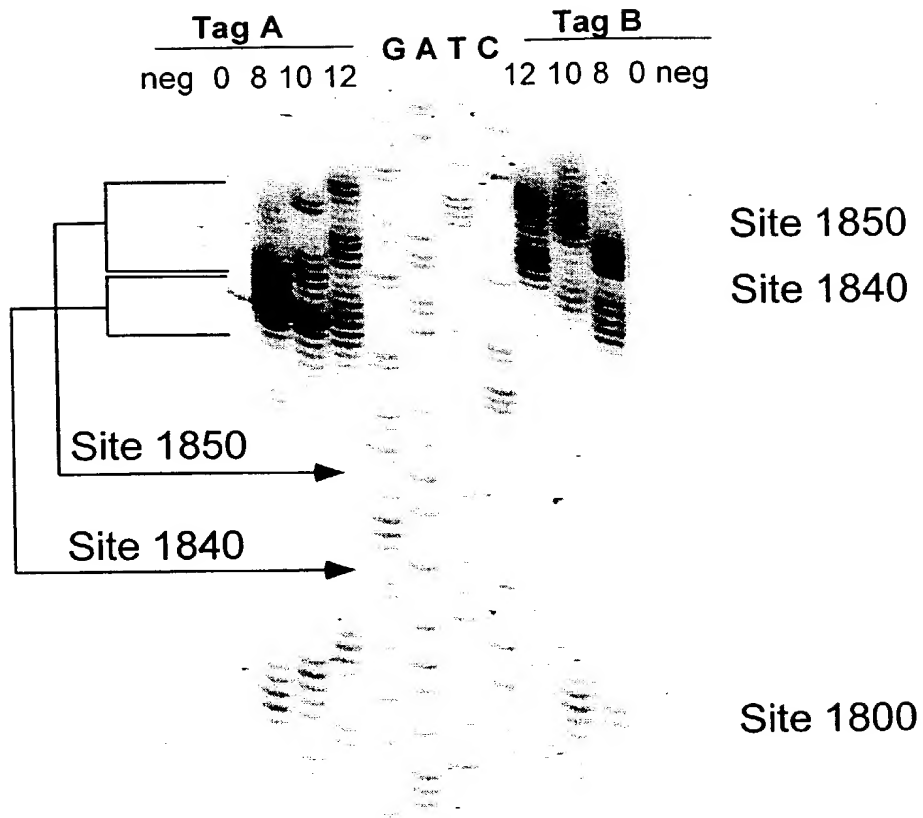
1910 UUCAGCUACC AUAAUGAUGC **AGAGAGGCAA** UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGC**AAAG**AG GGCACACAGC CAGAAAUUGC

2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G

FIGURE 56

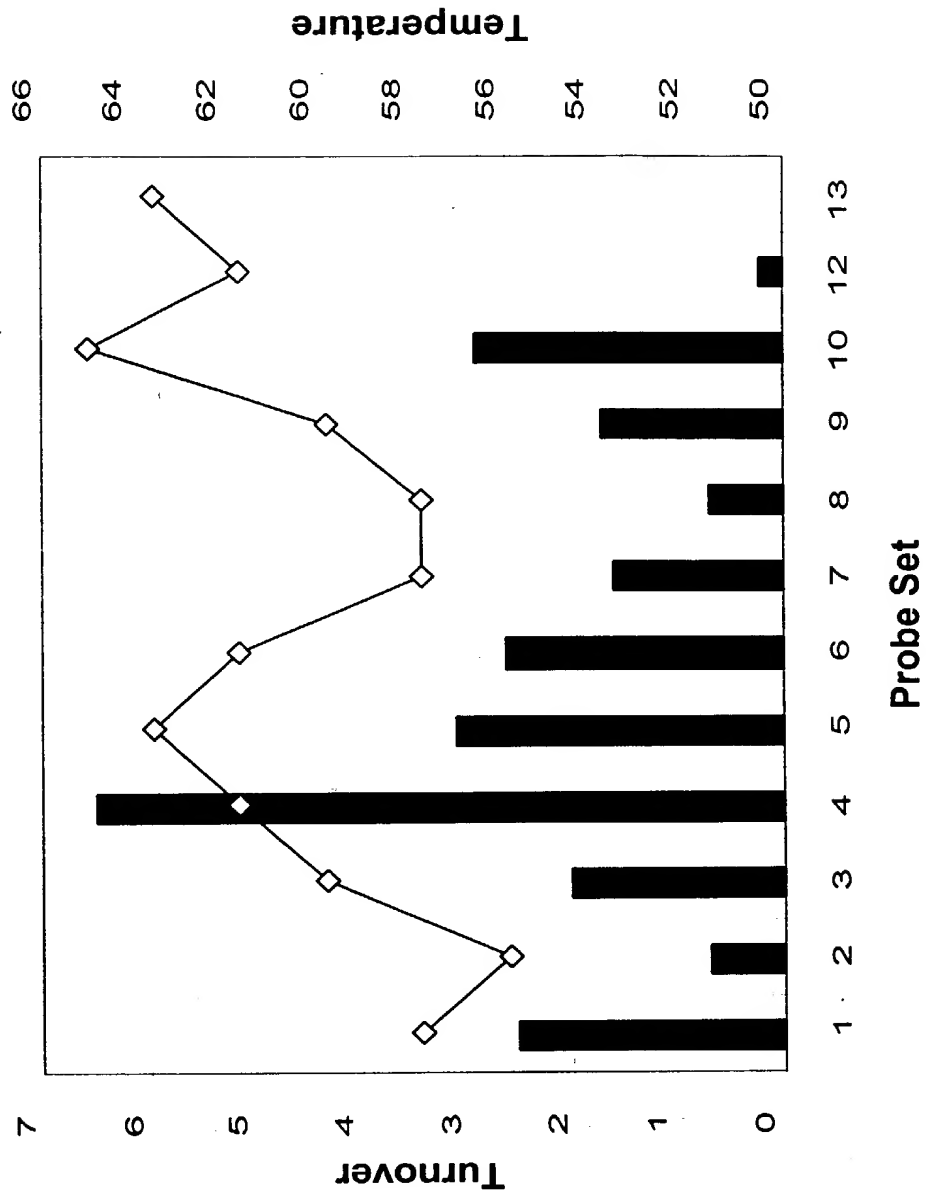


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FIGURE 57

(SEQ ID NO:188)	CGTATTCGTTCTCAAAACCGACTTGCT-5'	13
(SEQ ID NO:187)	AGGTATTCGTTCTCAAAACCGACT	12
(SEQ ID NO:186)	ACGGTATTCGTTCTCAAAACCGAC	10=11
(SEQ ID NO:185)	CCCGGTATTCGTTCTCAAAACCGA	9
(SEQ ID NO:184)	CGCCGGTATTCGTTCTCAAAACCG	8
(SEQ ID NO:183)	CGCCGGTATTCGTTCTCAAAACCG	7
(SEQ ID NO:182)	AGGCCGGTATTCGTTCTCAAAAC	6
(SEQ ID NO:181)	ATGGCCGGTATTCGTTCTCAAAAC	5
(SEQ ID NO:180)	ACTGGCCGGTATTCGTTCTCAAA	4
(SEQ ID NO:179)	ACCTGGCCGGTATTCGTTCTCAA	3
(SEQ ID NO:178)	ATCCTGGCCGGTATTCGTTCTCA	2
(SEQ ID NO:177)	ACTCCTGGCCGGTATTCGTTCTC	1
5'-CAUGCAGGAGUAGGAGACCCGCCAUAAGCAAGUUUGGCUAAGCAAUAGAG-3'	(SEQ ID NO:158)	
1 CAGTCCCTCATC	(SEQ ID NO:164)	
2 AGTCCCTCATCC	(SEQ ID NO:165)	
3 GTCCCTCATCCT	(SEQ ID NO:166)	
4 TCCCTCATCCTC	(SEQ ID NO:167)	
5 CCTCATCCTCC	(SEQ ID NO:168)	
6 CCTCATCCTCCT	(SEQ ID NO:169)	
7 CTCATCCTCCTG	(SEQ ID NO:170)	
8 TCATCCTCCTGG	(SEQ ID NO:171)	
9 CATCCTCCTGGG	(SEQ ID NO:172)	
10 ATCCTCCTGGGC	(SEQ ID NO:173)	
11 TCCTCCTGGGC	(SEQ ID NO:174)	
12 CCTCCTGGGCC	(SEQ ID NO:175)	
13 CTCCTGGGCCGAAA-FL-5'	(SEQ ID NO:176)	

FIGURE 58



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FIGURE 59

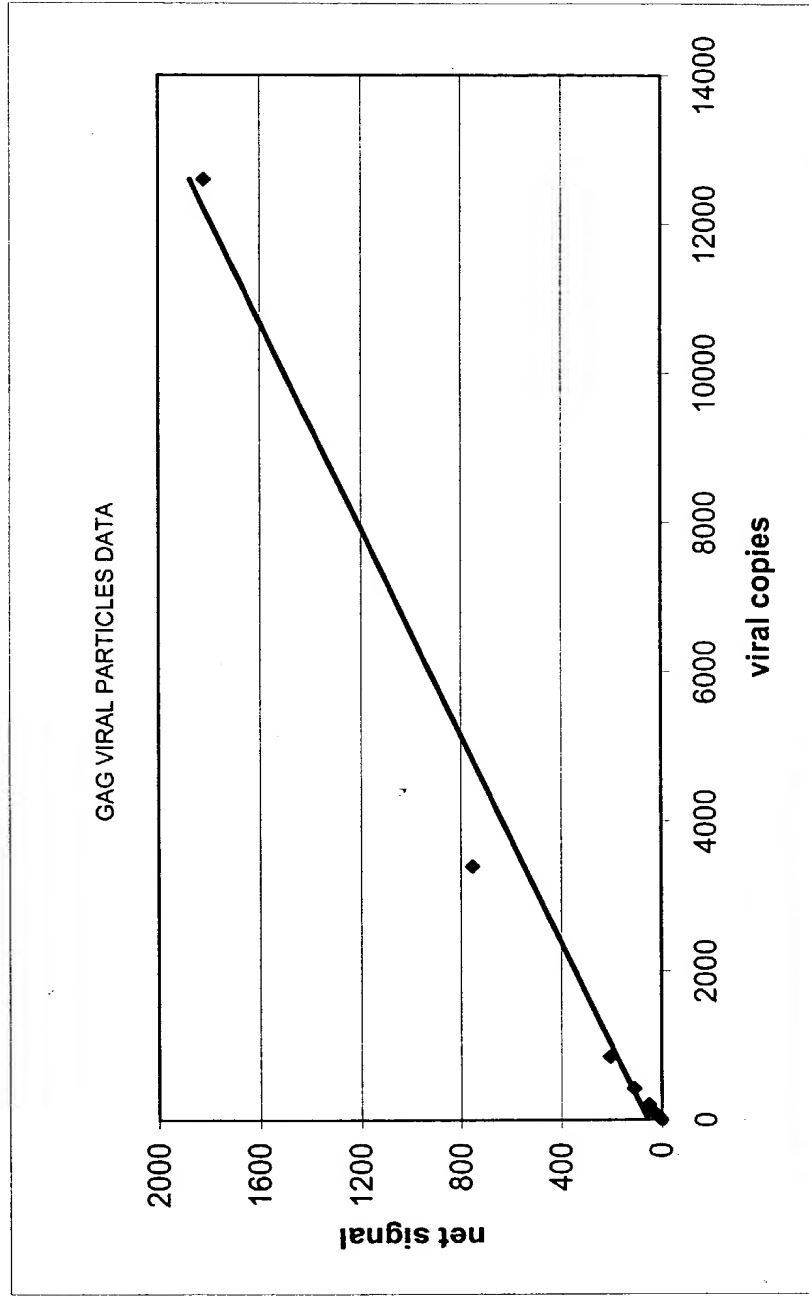
(SEQ ID NO:180)
 ACTGGCCCGGTATTCCGTTCTCAAA
 5' -CAUGUAGGGAGUAGGAGGACCCGGCCCAUAAGGCAAGAGUUUUGGCUGAAGCAAUGAG-3'
 (SEQ ID NO:158)
 TCCCTCATCCTCCTCCGCACTGCC-5'
 (SEQ ID NO:189)

5' -AGGAGTAGGAGGAGG-3'
 (SEQ ID NO:190)

(SEQ ID NO:191) (SEQ ID NO:193)
 5' -CCGTCACGCCTCC
 3' -TGGCAGTCCGGAGGTTGACGAAGAGGC-5'
 (SEQ ID NO:192)

Diagram showing a sequence alignment with a mutation site marked by a circle 'Q' and a circle 'F' with arrows pointing to the corresponding positions in the sequences above.

FIGURE 60



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FIGURE 61A

SEQ ID NO:159

primer 1
 3300 AGCUGGACUG UCAAUGACAU ACAGAAGUUA GUGGGGAAAU UGAAUUGGGC
 3350 AAGUCAGAUU UACCCAGGGA UUAAGUAAG GCAAUUAUGU AAACUCCUUA
 3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG
 3450 CUAGAACUGG CAGAAAACAG AGAGAUUCUA AAAGAACCAG UACAUGGAGU
 primer 2
 3500 GUAUUAUGAC CCAUCAAAAG ACUUAUAGC AGAAAUACAG AAGCAGGGGC
 3550 AAGGCCAAUG GACAUAUCAA AUUUUAUCAA AGCCAUUUA AAAUCUGAAA
 3600 ACAGGAAAAU AUGCAAGAAU GAGGGGUGCC CACACUAAUG AUGUAAAACA
 3650 AUUAACAGAG GCAGUGCAAA AAUAACCAC AGAAAGCAUA GUAAUAUGGG
 primer 3
 3700 GAAAGACUCC UAAAUUUAAA CUGCCCAUAC AAAAGGAAAC AUGGGAAACA
 3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU
 3800 UAAUACCCCU CCCUAGUGA AAUUAUGGUA CCAGUUAGAG AAAGAACCCA
 3850 UAGUAGGAGC AGAAACCUUC UAUGUAGAUG GGCAGCUAA CAGGGAGACU
 primer 4
 3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU AGAGGAAGAC AAAAAGUUGU

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[illegible]

4000 UAGCUUUGCA GGAUUC**GGGA** UUAGAAGUAA ACAUAGUAA ACAGACUCACAA

4050 UAUGCAUUAG GAAUCAUUCA **AGCACAACCA** GAUCAAAGUG AAUCAGAGUU

4100 AGUCAAUCAA AUAAUAGAGC AGUUAUUAAA AAAGGAAAAG GUCUAUCUGG

4150 CAUGGGUACC AGCACACAAA GGA**AUUGGAG** GAA AUGAACA AGUAGAUAAA

4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGA**UAA**

4250 **GGCCCAAGAU** GAACAUGAGA AAUAUCACAG UAAU**UGGAGA** GCAAUGGCUA

4300 GUGAUUUUAA CCUGCCACCU GUAGUAGCAA AAGAAAUAGU **AGCCAGCUGU**

4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG

4400 UCCAGGAAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC

4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUAU UAG**A**AGCAGA AGUUAUUCCA

4500 GCAGAAACAG GGCAGGAAAC AGCAUAAUUU CUUUUAAAAU **UAGCAGGAAG**

4550 **AUGGCCAGUA** AAAACAAUAC AU**ACUGACAA** UGGCAGCAAU UUC**ACCGGUG**

4600 CUACGGUAG GGCCGCCUGU UGGUGGGCGG GAAUCA**AGCA** GGAAUUUGGA

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FIGURE 61C

4650 AUUCCCUACA AUCCCCAAG UCA**AAGG**AGUA GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAGGAC AGGUAAGAGA **UCAGGC**UGAA CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG AAA**AGGGGGG**

4800 AUUGGGGGGU AC**AGUGCAGG** **GGAA**AGAAUA GUAGACAUAA UAGCAACAGA

4850 CAUACAAACU AAAGAAUAC AAAAACAAAU UACAAAAAUU CAAAUUUUC

primer 9

4900 GGGUUUAUUA CAG**GGACAGC** AGAAAUCCAC UUUGG**AAAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAAGG** GGCAGUAGUA AUACAAGAU AUAGUGACAU

5000 AAAAG**UAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAAC

5050 AGAUGGCAGG UGAUGAUUGU G

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TOST 90 5462860

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FIGURE 62

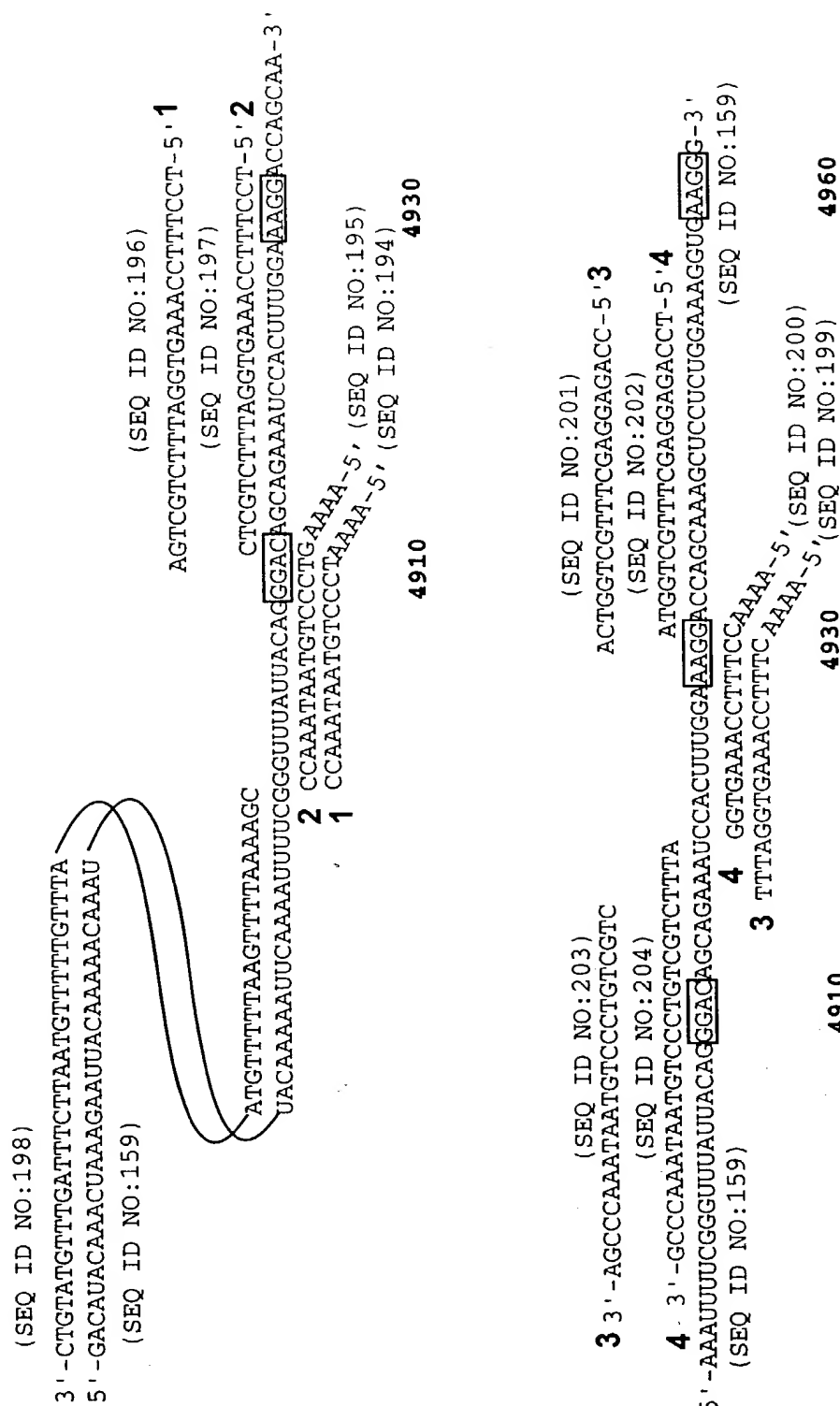
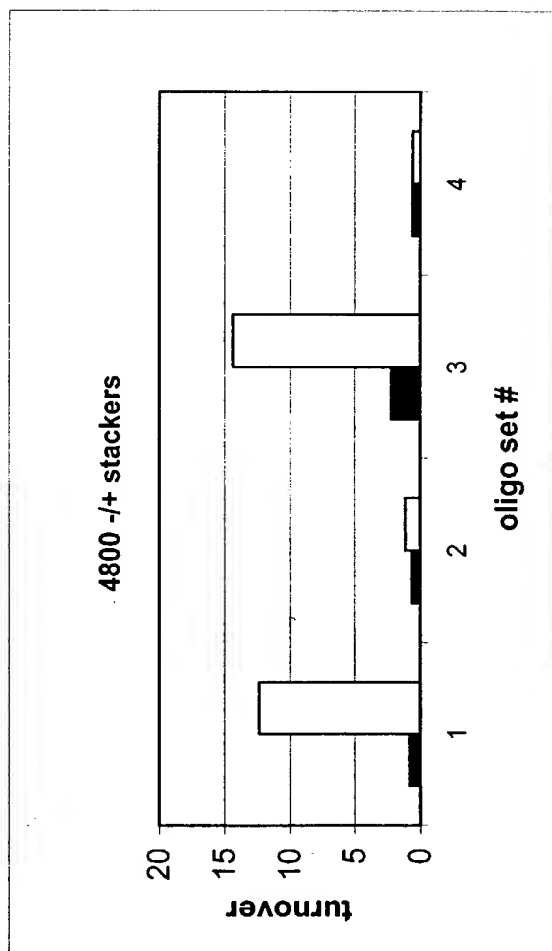


FIGURE 63

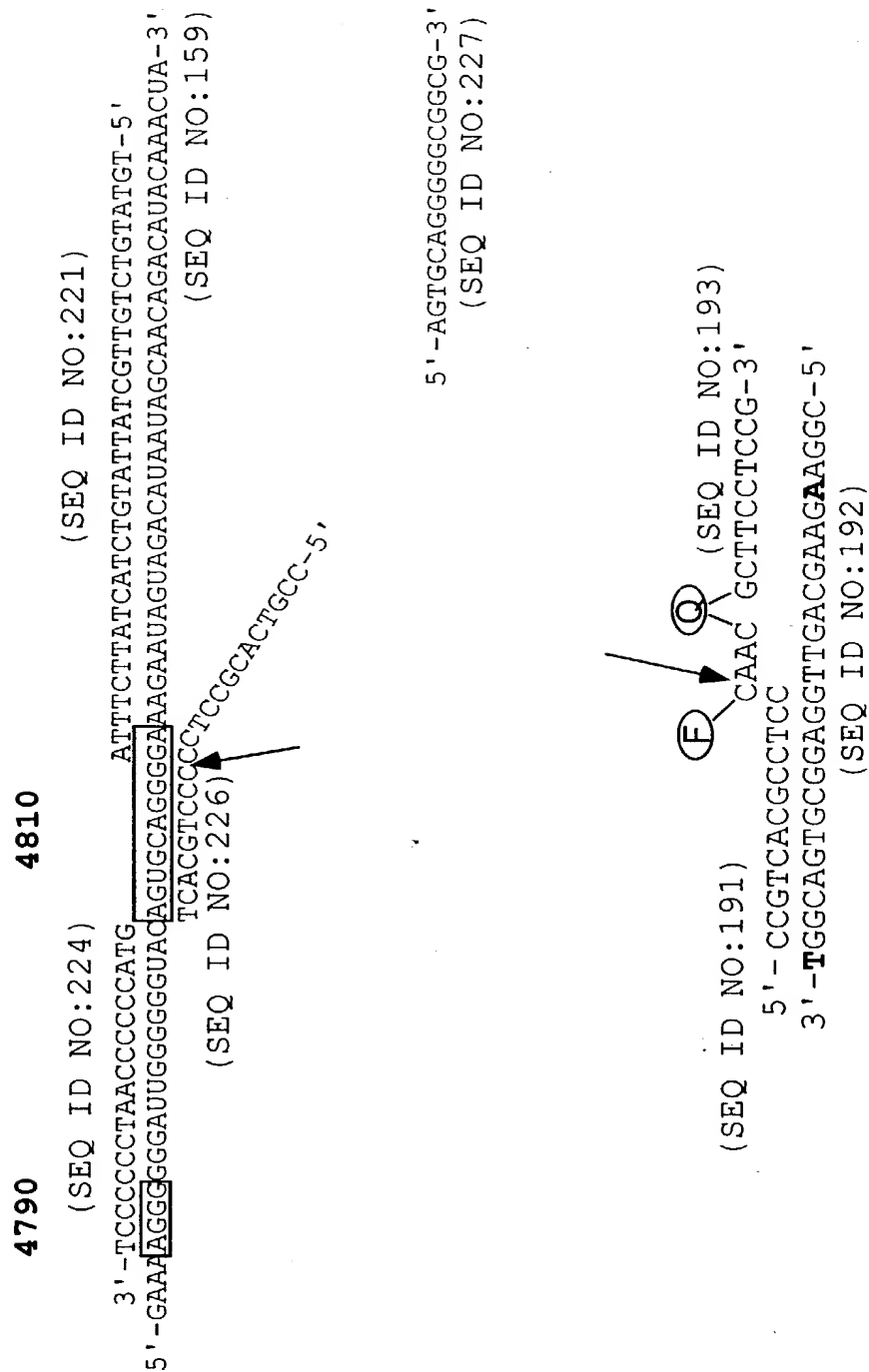
5 3'-TCCTGGTCGTTTCGAGGAGA (SEQ ID NO:213)
 6 3'-CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:214)
 5'-GAAAGGACCAGCAAGCUCUCUGGAAAGGUAAGGCGCAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3' (SEQ ID NO:209)
 4930 ACCCGTCATCATTTATGTTCTATTATCACTGTATTTT-5' 5
 6 3'-CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:210)
 5'-GAAAGGACCAGCAAGCUCUCUGGAAAGGUAAGGCGCAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3' (SEQ ID NO:210)
 4960 CTTTCCACTTCCAAA-5, (SEQ ID NO:206)
 5 CTTTCCACTTCCAAA-5, (SEQ ID NO:205)
 4960 CTTTCCACTTCCAAA-5, (SEQ ID NO:205)
 7 3'-TCGAGGAGACCTTTCCAC (SEQ ID NO:215)
 8 3'-TCGAGGAGACCTTTCCACT (SEQ ID NO:216)
 5'-GAAAGGACCAGCAAGCUCUCUGGAAAGGUAAGGCGCAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3' (SEQ ID NO:211)
 4930 TCCCGTCATAAAA-5, (SEQ ID NO:208)
 7 TCCCGTCATAAAA-5, (SEQ ID NO:207)
 4960 TCCCGTCATAAAA-5, (SEQ ID NO:208)
 7 TCCCGTCATAAAA-5, (SEQ ID NO:207)

FIGURE 65



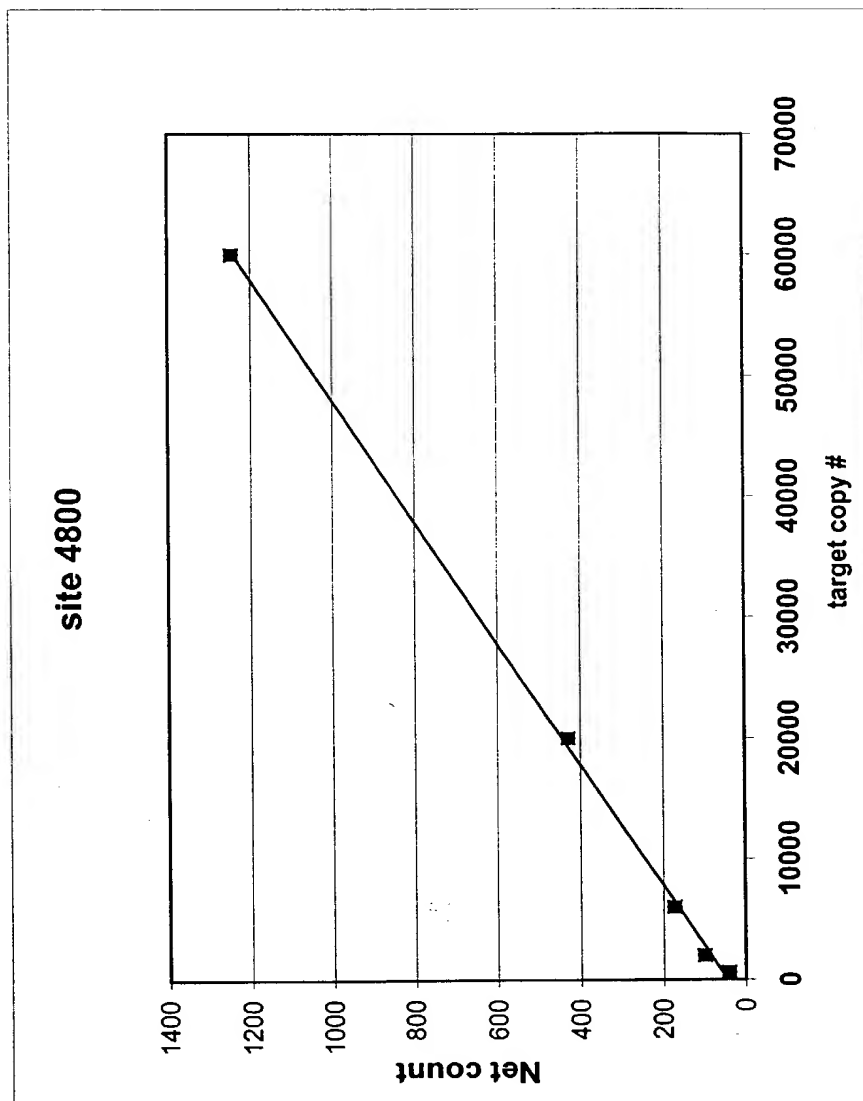
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FIGURE 66



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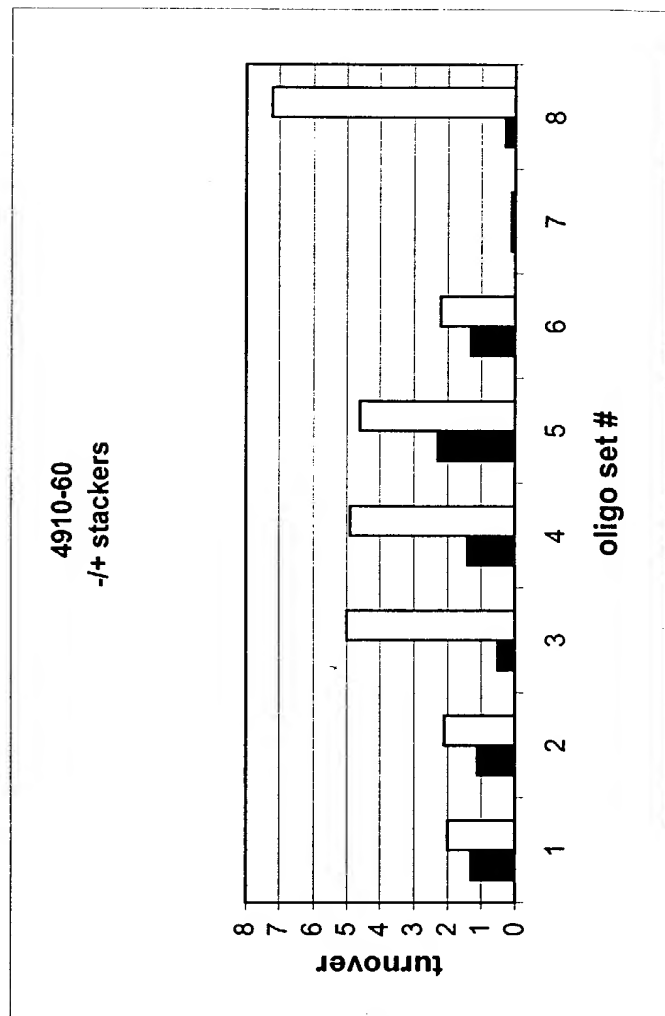
FIGURE 67



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FIGURE 68

FIGURE 68



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FIGURE 69

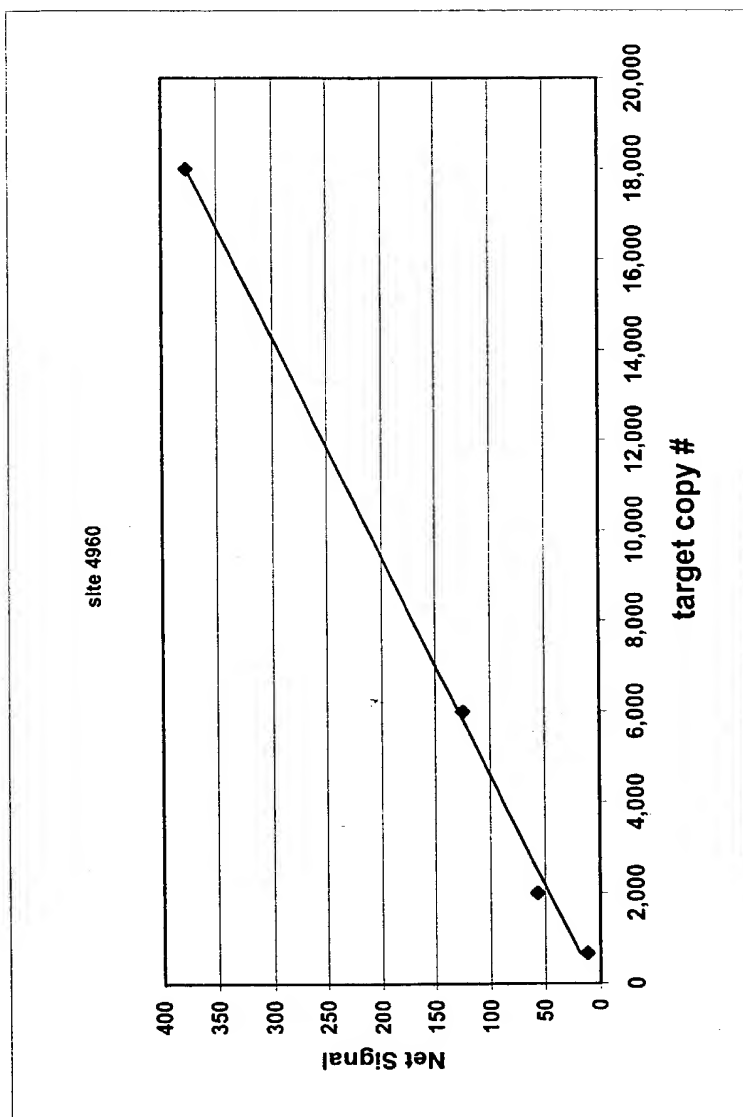
(SEQ ID NO:213) 4960 (SEQ ID NO:209)
 3'-TCCTGGTCGTTTCGAGGAGA ACCCGTCATCATTAATGTTCTATTATCACTGTATTT-5'
 5'-GAAGGACCAGCAAAGCUCCUCUGGAAAGGUGAAGCGGCAGUAGUAAUACAAGAUAGUGACAUAAAAAGUAGU-3'
 CCTTCCACTTCCTCCGCACTGCC-5' (SEQ ID NO:159) 5000
 4930 (SEQ ID NO:228)

5'-GGAAAGGTGAAGGAGGC-3'
 (SEQ ID NO:229)

(SEQ ID NO:191) (F) (Q) (SEQ ID NO:193)
 CAAC GCTTCCTCCG-3'
 5'-CCGTCACGCCTCC
 3'-TGGCAGTCCGAGGTTGACGAAGAAGGC-5'
 (SEQ ID NO:192)

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FIGURE 70



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FIGURE 71

Human PSP94

383-31-1 5'-TET-CCTGCTTATCACAATGAA-3' (SEQ ID NO:230)

383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGGGCAGCGUUGUGAUCUUUGCCACCUUCGUGA
CUUUAUGCAAUGCAUCAUGCUAUUUCAUACCUAUGAGGGAGUCCAGGAGAUUCAACCA
GGAAUGCAUGGAUCUCAAGGAAACAAACACCCAAUAAACUCGGAGUGGCAGACUGAC
AACUGUGAGACAUGCACUUGCUACGAAACAGAAAUUUAUGUUGCACCCUUGUUUCUAC
ACCUGUGGGUUAUGACAAAGACAACUGCCAAAGAAUCUUCAAGAAGGAGGACUGCAAGU
AUAUCGUGGUGGAGAAGAAGGACCCAAAAAAGACCUGUUCUGUCAGUGAAUGGAUAAUC
UAAUGUGCUUCUAGUAGGCACAGGGCUC³CCAGGCCAGGCCUCAUUCUCCUCUGGCCUCUA
AUAGUCAAAUGAUUGUGUAGCCAUGCCUAUCAGUAAAAAGAUUUUUG

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FIGURE 72

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)
520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAAUGCAGAUUUUCGUGAAAACCCUUA CGG GGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAAUGUA AAGGC CAAGAUCCAGGAUAAGGAAGGAAU
UCCUCCUGACAGCAGAGACUGAUCUUUCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUCAUCUUGUGUUGAGACUU CGUGGUG G
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAA GCU GGCUGUCCUGAAAUAUUUAUAAGGUGGAUGAGAAUGGCCAAAUAUAGUC
GCCUUCGUCGAGAGUGCCCUUCUGAUGAUGUGGUGCUGGGGUGUUUAUGGCAAGUCACU
UUGACAGACAUUAUUGUGGCAAAUGUUGUCUGA

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FIGURE 73

HCV-1a 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUC
UUGGAU[AAACCC]GCUCAAUGCCUGGAGAUUU[GGG]CGUG[CCC]CCGCAAGACUGCU[AGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

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FIGURE 74

HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAU[CAACCC]GCUCAAUGCCUGGAGAUUU[GGG]CGUG[CCCC]CG[CG]AGACUGCU[AGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

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FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)

898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)

898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)

898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCCCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAUUGCCGGGAAGACUGGGUCCUUUC
UUGGAUAAACCCACUCUAUGCCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUCGUAGACCGU[GCACCAUGAG]

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FIGURE 76

HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGC
CUAGCCAUGGCGUUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUCGCUGGGGUGACCGGGUCCUUUC
UUGGAA[CAACCC]GCUCAAUACCCAGAAAUUUGGGCGUG[CCCC]CGCGAGAUAC[UAGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

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FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aaggggaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagtttgcaagaaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtcctgg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagttttggatctttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caatactgcagatggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgtttctgcacaga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)

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T05T90 5463360

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA
GUUUGCAAGAAACAGGUGCUUAACACUAAUUCACCUCCUGAACAAGAAAUAUGGGCUGU
GACCGGAAUCUGUGGGCUCAUCGUGGGCUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG
AGGUAUUCUAAUGCCA GUUGGAGACCUGCUUAUCCA GAAGACAAUUA AAAAGCAAGUUG
UCCUCGAAGAAGGUACAAUUGCUUUUAAAAUUGGGUAAAA CAGGCACAGAAGUUUAC
AGACAGUUUUGGAUCUUUGAUGUGCAAAA UCCACAGGAAGUGAUGAUGAACAGCAGCAA
CAUUCAAGUUAAGCAAAGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA
AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCCUGCAGCCCAAUGGUGCCAUUC
UUUGAACCUCACUAUCAGUUGGAA CAGAGGCUGACAACUUCACAGUUCUCAUCUGGC
UGUGGCAGCUGCAUCCC AUAUCUAUCAAAAUCAAUUUGUUCAAAUGAUCCUCAAUUCAC
UUAUUACAAGUCAAAAUCUUCUAUGUCCAAGUCAGAACUUUGAGAGAACUGUU AUGG
GGCUAUAGGGAUCCAUUUUUGAGUUUGGUUCCGUACCCUGUUACUACUACAGUUGGUCUG
UUUUAUCCUUACAACAUAUCUGCAGAUGGAGUUUAUAAAGUUUUCAAUGGAAAAGAUAA
CAUAAGUAAAGUUGCCAUAAUCGACACAUUAUAAAGGUAAAAGGAAUCUGUCCUAUUGGG
AAAGUCACUGCGACAUGAUUAAUGGUACAGAU GCA GCCUCAUUCACCUCUUUGUUGAG
AAAAGCCA GGUAUUGCAGUUCUUUUCUUCUGAUAUUUGCAGGUCAAUCUAUGCUGUAUU
UGAAUCCGACGUUAAUCUGAAAGGAAUCCUGUGUAUAGAUUCGUUCUCCA UCC AAGG
CCUUUGCCUCUCCAGUUGAAAA CCCAGACAACUAUUGUUU CUGCACAGAAAAAUUAUC
UCAAAAAAUUGUACAUCAUAUGGUGUGCUAG ACAUCAGCAAUGCAAAGAAGGGAGACC
UGUGUACAUUUCACUCCUCAUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA
UGGAUUAACCCAAAUGAAGAAGACAUAGGACAUACUUGGAUAUUAACCUAUAA CUG
GAUUCACUUUACA AUUUGCAAAACGGCUGCAGGUCAACCUAUUGGUCAAGC CAUCAGAA
AAAAUUCAAGUAUUAAGAAUCUGAAGAGGAACUAUAUUGUGCCUAUUCUUUGGCUAA
UGAGACUGGGACCAUUGGUGAUGAGAAGGCAAA

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FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01 5'-ATGGGGTTTGTAAAGTTG-3' (SEQ ID NO:260)
 761-47-02 5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3' (SEQ ID NO:261)
 937-05-01 5'-TET- atgggggtttgttaaagtt-3' (SEQ ID NO:262)
 937-05-02 5'-TET- gaagacgacgagagg-3' (SEQ ID NO:263)
 937-05-03 5'-TET- ggatgatagttcgtgtg-3' (SEQ ID NO:264)
 937-05-04 5'-TET- gctgcagcatattgta-3' (SEQ ID NO:265)
 937-05-05 5'-TET- ctgctatttggtatgca-3' (SEQ ID NO:266)
 937-05-06 5'-TET- gcagaagtacatcgga-3' (SEQ ID NO:267)
 937-05-07 5'-TET- gacatgatggaggaga-3' (SEQ ID NO:268)
 937-05-08 5'-TET- agaagaaggatcgga-3' (SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUGUUAAGUUGUUAAGAAUAAGGCUCACUUUAAGAGAUACCAAGUGAAAUU
 UAGAAAGACGACGAGAGGGUAAAACUGAUUAUUAUGCUCGGAAACGCUUGGUGAUACAAG
 AUAAAAUAAAUACAAACACCCAAAUAACAGGAUGAUAGUUCGUGUGACAAACAGAGAU
 AUCAUUGUCAGAUUGCUUAUGCCCUGAUAGAGGGGGGAUAUGAUAGUCUGCGCACGUUA
 UGCACACGAACUGCCAAAUAUGGUGUGAAGGUUGGCCUGACAAAUUAUGCUGCAGCAU
 AUUGUACUGGCCUGCUGCUGGCCCGCAGGCUUCUCAAUAGGUUGGCAUGGACAAGAUC
 UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAGUGGAAAGCAUUGAUGGUCAG
 CCAGGUGCCUUCACCUGCUAAUUGGAUGCAGGCCUUGCCAGAACUACCACUGGCAAUAA
 AGUUUUGGUGCCUGAAGGGAGCUGUGGAUGGAGGCUUGUCUAUCCUCACAGUACCA
 AACGAUUCCUUGGUUAUGAUUCUGAAAGCAAGGAUUUAAUGCAGAAGUACAUCGGAAG
 CACAUCUUGGCCAGAAUGUUGCAGAUUAACUUGCGUACUUAAUGGAAGAAGAUGAAGA
 UGCUUACAAGAAACAGUUCUCUCAAUACAUAAGAACAGGUAACUCCAGACAUGAUGG
 AGGAGAUGUAUAAGAAAGCUAUGCUGCUAUAAGAGAGAAUCCAGUCUAUGAAAGAAG
 CCCAAGAAAGAAGUAAAAAGAGAGGUGGAACCGUCCAAAAUGUCCCUUGCUCAGAA
 GAAGGAUCGGUAGCUAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
 AGAGCUAAACCCAGC

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FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA

Oligonucleotides

726-39-01	5'-GCTCAAGAATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTTTGC-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtggaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggaccctatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caaggggtgtttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

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FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUGC
CCGUCCC UUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAAC[GAG]GUCCUC
AACGGCCAGAAGCCAGUAGU[CCGGG]AGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA
AAAGGUCAACAUCACCUUCAUGA[CAACGACACC]GUGUCCUUCGUGGAGAA[CCGCAGC]C
UCCAUUUCCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA
UCUUGGUCCUGGGGGGCU CGAUAUUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG
AUGACCUUGGCGCUGGUCACCAUGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA
GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUUUUCUACAACACGUACCUC CAGACAU
GCUUCCCAUAAAGGGCAAUUUGGCCUGUUUGUUGGAUGAACAACUCGAAUUC[UGG]GG
UCUUCACUGUCUUC[ACGG]GCGUCCAGAAUUUC[AGCA]GGAUCCAUCUGGUGGACAAAUGG
AACGGACUCAGCAAGAUCGAUUAU[UGGCAUUCAGAGCA]GUGUAACAUGAUCAA[UGG]GAC
U[UCCGG]GCAGAUG[UGGGC]ACCCUUCA[UGACACC]CGA[AUCCUC]GCUGGAAUUCUUCAGCC
[CGGA]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU
CCCACGUAUCGCUUC[ACGGCC]CCCGAUACUCUGUUUGCCAACGGGUCCGUCUACCCACC
CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU
UGGUGCGCCUCUGUUUCUCUCCACCCCCACUUUUAC[AACGCCGAC]CCUGUGUUGUCAG
AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUCCUUGUCCUAGACAUCCA[U]
[CCGGU]CACUGGGAUCCCCAUGAACUGUUCUGUGAAGAU[GCAGC]UGA]GCCUCUACAUCAA
AUCUGUCAAGGGCAUCGGGCAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG
GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU
GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGCUUGGAGGCCUCCU
GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAAAUGCUUUUUGUUUUGGA
GUGGUAGUAAAAGGGCUCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCUGA
UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA
CUAUAAG[CCCC]CCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCG
CUUCUUGAGGACUCUCUCAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAUGU
CACACCUGUCCGCACGCACGGCACAUGGAUGCCCACGCAUGUGCAAAAACAACUCAGGGA
CCAG

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FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

761-57-01	5'-taatacgactcactatagggacggaagtccaagagcatcactg-3'	(SEQ ID NO:286)
761-57-03	5'-gcagggtacctggtccgta-3'	(SEQ ID NO:287)
781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
781-65-02	5'-TET-aatggcttctttggg-3'	(SEQ ID NO:289)
781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
781-65-04	5'-TET-tacttccgcacgcgc-3'	(SEQ ID NO:291)
781-65-05	5'-TET-cttcttccctagttgtg-3'	(SEQ ID NO:292)
781-65-06	5'-TET-tgcctggccgt-3'	(SEQ ID NO:293)
781-65-07	5'-TET-gactctactaagaaccca-3'	(SEQ ID NO:294)
781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
781-85-02	5'-TET-tgattacccccgagg-3'	(SEQ ID NO:298)
781-85-03	5'-TET-acgctgttttcctg-3'	(SEQ ID NO:299)
781-85-04	5'-TET-tgagacacctgtacaa-3'	(SEQ ID NO:300)
781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
781-85-06	5'-TET-caagcgagggagag-3'	(SEQ ID NO:302)

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[illegible]

GGAAGUCCAAGAGCAUCACUGACAUCUACCUCUGAACCUGGCCUUGAGCGACCAGCAGCUC
UUUGUGGCCACUUUGCCCUUCUGGACUCACUACCUCAUCAGCCAUGAGGGGCCUCCACAA
CGCCAUGUGCAAGCUACGACUGCUUUCUUCUUCAUUGGCUUCUUUGGGGCAUAUUCU
UCAUCACCUGUCAUAGCAUCGACCGGUACCGCCAUCGUCUGGGCCCAACUCCAUG
AAACAACGGACAGUGCAAACACGGCGUCACCAUCAGUCUGGGCGUCUGGGCGGCGGCCAU
CUUAGUGGCGUCGCCCCAGUUAUGUUCACAAAGAGAAAGGACAACGAAUGUUUGGGUG
AUUACCCCGAGGUCCUGCAGGAAAUUGGCGCCGUGCUCGCAACUCGGAGGUCAACAUC
CUGGGCUUCGUCCUGCCCUUGCUUAUCAUGAGCUUUUGCUACUUCCGCAUCGUCCGGAC
GCUGUUUUCUGCAAGAACCAGGAAGAAGGCCAGAGCCAUUAGGCUCAUCCUCUUGGUGGU
UGUUGUCUUCUCCUCUUUGGACGCCUUAACAACAUCGUGAUUUUCCUGGAGACUCUCA
AAUUCUACAACUUCUUCUCCUAGUUGUGGCUGAAGAGGGACUGAGGUGGGCCCUAGU
GUGACGGAGACAGUGGCGUUUAGCCACUGCUGCCUACAACCCCUUAUCUACGCUUUCGC
UGGGGAAAAGUUCAGAAGGUACUGAGACACCUGUACAACAAGUGCCUGGGCCGUCUGU
GCGGUCGUCCUGUCCACGCGGCUUCUCAACAGAGUCCAGAGGAGCAGGCAGGACAGC
AUUCUGAGCAGCUUGACUCACUACACAAGCGAGGGAGAGGGAUCUCUCCUGCUCUGAAGG
GUCUCCCCGACCCGACUCUACUAAGAACCCAGAGUCCUGCAUCUGACUCUGUGUAAUG
AAAACAGAUUCACCCCG
CUCCUCCUGCAUUUUAUGUGCAAGAAAUACGGACCAGGUACCUGC

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FIGURE 81A

Human Interleukin-1 beta (IL-1 β) Oligonucleotides

720-82-01 5'-
gtaatttaatacgaactcactataggggaaggtgcagttttgcccaaggagtgctaaag-3'
(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaacatcat-3'
(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)

781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)

781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)

781-50-04 5'-TET-cattgtaccatgaaatatcc-3' (SEQ ID NO:309)

781-50-05 5'-TET-gaactttaatttcaggaattg-3' (SEQ ID NO:310)

781-50-06 5'-TET-ccctagtctgctagc-3' (SEQ ID NO:311)

781-50-07 5'-TET-ttcaagtgtaacttattaacc-3' (SEQ ID NO:312)

781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)

781-72-02 5'-TET-tgcagttttgccaaag-3' (SEQ ID NO:314)

0000045-061504
TET-acttccaagctggc-3'

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FIGURE 81B

Human Interleukin-1 beta (IL-1 β) (GenBank Accession #
M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGAAUGAUGGCUUAUUAAGUGGCAAUGAGGAUG
ACUUGUUCUUUGAAGCUGAUGGC CCUAAACAGAUGAAGUGCUCUCCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUC CCGACCAC CACUA CAGCAA GGG
CUUCAGGCAGGCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUU C
CCUGCC CACAGACCUUCCAGGAGAAUGA CCUG AGCACCUCUUCUCCUUAUCUUUGAA
GAAGAACCUAUCUUCUUCG ACACAUGG GAU AACGA GGCUUAUGUG CACGA UGCACCUGU
ACGAUC ACUGAACUGCACGCUCCG GGACUCACAGCAAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCU CUCC ACCUC CAGGGACAGGAUAUGGAGCAACAAGUGGUGUUC
UCCAUGUCCUUGUACAAGGAGAAGAAAGUAAUGACAAAUAACCUGUGGCCUUGGGCCUC
AAGGAAAAGAAUCUGUAC CUGUCCUGCG UGUUGAAAGAUGAUAAAGCCCACUCUACAGCU
GGAGAGUGUAGAUC CAAAAAUUACCCAAAGAAGAAGUUGGAAAAGCGAUUUGUCUUCAA
CAAGAUAGAAUCAAU AACAAAGCU GGAAUUGAG UCUG CCCAGUCCCCAACUGGUAC A
UCAGCACC UCUCAAGCAGAAAA CAUGC CCGUCUCCUGGGAGGGACCAAAG GCGG CCAG
GAUAUAACUGACUUC ACCA UGCAAUUUGUGUCUCCUAAAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAAUCC CUAGGGCU GGCAGAAAGGGAACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUUCCUGUUGUCUACACCAUGCCCAACUGCCUGCCUU
AGGGUAGUGCUAAGAGGAUCUCCUGUCCA UCAGCCA AGGACAGUCAGCUCUCUCCUUU CA
GGGCCAAUCC CCAGC CCUUUUGUU GAGCCAGGCCUCUCUCAC CUCUCCUACUCACUU AA
AGCCCGCC UGACAGA AACACGG CCACAUUUGGUUCUAAGAAACCCUCUGUCAUUCGCU
CCCACAUUCUGAU GAGCAACCGCU UCCCUAUUUUAUUUAUUUUGUUUGUUUUUA
UUCAUUGGUCUAAUUUAUU CAAAGGGGGC AAGAAGUAGCAGUGUCUGUAAAAGAGCCUA
GUUUUUAAUAGCUAUGGAAUCAAUUCAAUUGGA CUG GUGUGCUCUCUUUAAAUCAAGU
CCUUUAA UUAAGAC UGAAAAUAU AUAAGCU CAGAUUAUUU AAAUG GGAAUAUUUAUAA A
UGAGCAAAUAUCAUACUGUUA

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FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01	5'-TET-GCATCGTTTTGGGTTCTCTT	(SEQ ID NO:316)
448-59-02	5'-TET-ACTTTAAAGATGACCAGAGC	(SEQ ID NO:317)
448-79-01	CACATTGTTCTGATCATCTG	(SEQ ID NO:318)
448-79-02	CGGTAAGTGAATGTC	(SEQ ID NO:319)
448-79-03	TAGTAAGTGAATGTC	(SEQ ID NO:320)
448-79-04	GACATTCAAGTCAGTTACCG	(SEQ ID NO:321)
498-20-01	AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG	(SEQ ID NO:322)
498-20-02	AATTTAATACGACTCACTATACGGTAAGTGAATGTC	(SEQ ID NO:323)
498-20-03	5'-TET-CACATTGTTCTGATCATCTG	(SEQ ID NO:324)
498-20-04	5'-TET-CGGTAAGTGAATGTC	(SEQ ID NO:325)
498-40-01	5'- AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA	(SEQ ID NO:326)
498-40-02	5'- AGTAATTTACGACTCACTATAGGGACGGTAAGTGAATGTCCAAC	(SEQ ID NO:327)
498-84-01	5'-TET-CATTCAGATGTAGCG	(SEQ ID NO:328)
498-84-02	5'-TET-GACTCATCAATCAAA	(SEQ ID NO:329)
498-84-03	5'-TET-GATTACAAGGCTTTA	(SEQ ID NO:330)

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FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCaucUGAAGAUCAGCUAUUAGAAGAGAAAGAUcAGUUAAGUCCUUU
GGACCUGAUCAGCUUGA[UACAA]GAACUACUGAUUUCAACUUCUUUGG[CUUAAU]UCUCUC
GGAAACGAUGAAAUAUACAAGUUUAUcUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC
UCUUGGCUGUUACUGCCAGGACCCAUAUGUA[CAAGAAGC]AGAAAACCUUAAGAAAUAUU
UUAA[UGCAG]GUCAUUCAGAUG[UAGC]GGAUAAUGGAACUCUUUUUCUAGGCAUUUUGAAG
AAUUGGAAAGAGGAGAGUGACAGAAAAUAUUG[CAGA]GCCAAAUUGUCUCCUUUUACUU
CAAACUUUUUAAAAACUUUAAAGA[UGACCAGA]GCAUC[CAAAAG]AGUGUGGAGACCAUCA
AGGAAGACAUGAAUGUCAAGUUUUUCAUAGCAACAAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUUAUUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGU[CGCCAG]CAGCUAAA[ACAGGGAAGCGAAAAAG]GAGUCAG
AUGCUGUUUCGAGGUCGAAGAGCAUCCAGUAAUGGUUGUCCUGCCUACAAUAUUUGAAU
UUUAAAUCUAAAUCUAUUUAUUAAUAUAACAUAUUUAUAUGGGGAUAUAUUUUUAGAC
UCAUCAAUCAAUAAGUAUUUAUAAUAGCAACUUUUGUGUAAUGAAAUGAAUAUCUAUU
AAUAUAUGUAUUUAUUUAUAAUCCUAUAUCCUGUGACUGUCUCACUUAUCCUUUGUUUU
CUGACUAAUUAAG[GCAA]GGCUAUGUGAUU[ACAAG]GGCUUUUAUC[UCAGGG]GCCAACUA[GGCA]
[G]CCAACCUAAG[CAAGAUC]CAUGGGUUGUGUGUUUAUUUCACUUGAUGAUACAAUGAAC
ACUUAUAAGUGAAGUGAUACUAUCCAGUUACUA

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FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION #
AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAAUAAAUUCAGAUUGC
GACACUGUCAAAUUGC GGGGAAGCCCUAAAGAUUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAUAGCCCUGGGUAUAGUAACAAUGUUGAAUAUGAAUCUUUU
GCGAGAUGAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGA CUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUUCUUGCAGUGCUAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION #
X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUCCAGAAAUGGGCCGCGGUGUUUUUGACCUGC
UAGUC GAUCUGGCCAGACGUUAUCUGUGGGUGGCCAGCGGCGACUAACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGGUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCG UAGAG
CAGGAAAGGUAUGGGCUGGCUCUCUGAGUCGGCUAA GGUACGUGCCG UCCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

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FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUCUAAGUG
AUAAUACCGUUGUUUUUUUAGUGGGUAUUCUUUUACGCUUUCGUAGGAGCGAGUCCCAC
ACUCUUGGAAGCAAUCCGGGGUAGUGCCUAAACGCAUUUCUUAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCCGGA
GCUCGCUCCCUUGGCUUCCCUUAUAUAUUUUAACAUCAGAAACAGACAUUAAACAUCUA
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAAUCUCGGGGGUCUU
CCGAUCCUAAUCCAUGAUGAUUACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG

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TOSTED" 54628860